

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2000, 20:19:38 ; Search time 50.07 Seconds
(without alignments)
4863.166 Million cell updates/sec

Title: US-08-305-518-7

Perfect score: 1610
Sequence: 1 CGGATGAGCCCTGTGACT.....GCTTCACATTAGAGCCG 1610

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620727 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/5E.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCRTUS.COMB.seq:*
7: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	1610	100.0	1610	5	US-08-889-108-7	Sequence 7, Appli
2	1610	100.0	1610	6	PCT-US94-10358-7	Sequence 7, Appli
3	1123.8	69.8	1618	5	US-08-889-108-1	Sequence 1, Appli
4	1123.8	69.8	1618	5	US-08-889-108-3	Sequence 3, Appli
5	1123.8	69.8	1618	6	PCT-US94-10358-1	Sequence 1, Appli
6	1123.8	69.8	1618	6	PCT-US94-10358-3	Sequence 1, Appli
7	443.2	27.5	1829	4	US-08-411-859-1	Sequence 1, Appli
8	443.2	27.5	2272	5	US-08-147-592A-3	Sequence 3, Appli
9	416.4	25.9	1410	5	US-08-147-592A-1	Sequence 1, Appli
10	385.6	24.0	1000	5	US-08-147-592A-11	Sequence 11, Appli
11	363.8	22.6	1567	5	US-08-889-108-16	Sequence 16, Appli
12	363.8	22.6	1567	6	PCT-US94-10358-16	Sequence 16, Appli
13	363.8	22.6	2706	3	US-08-454-549-1	Sequence 1, Appli
14	363.8	22.6	2706	3	US-08-454-552-1	Sequence 1, Appli
15	361.8	22.5	1452	5	US-09-170-331-3	Sequence 3, Appli
16	360.6	22.4	2706	5	US-08-676-351-1	Sequence 1, Appli
17	357.4	22.2	1330	5	US-08-147-592A-5	Sequence 5, Appli
18	356.4	22.1	1452	1	US-08-149-093A-3	Sequence 3, Appli
19	356.4	22.1	1452	1	US-08-911-245-3	Sequence 3, Appli
20	356.4	22.1	1452	2	US-08-553-058C-3	Sequence 3, Appli
21	356.4	22.1	1452	3	US-08-514-451A-3	Sequence 3, Appli
22	336	20.9	2600	2	US-08-147-949A-1	Sequence 1, Appli
23	201.8	12.5	1244	1	US-07-816-283-7	Sequence 7, Appli
24	201.8	12.5	1244	2	US-08-417-103-7	Sequence 7, Appli
25	199.4	12.4	1147	2	US-08-417-103-15	Sequence 15, Appli
26	199.4	12.4	1351	1	US-07-816-283-5	Sequence 5, Appli

27	199.4	12.4	1351	2	US-08-417-103-5	Sequence 5, Appli
28	187.2	11.6	1265	1	US-07-816-283-3	Sequence 3, Appli
29	187.2	11.6	1265	2	US-08-417-103-3	Sequence 3, Appli
30	184	11.4	1205	2	US-08-417-103-13	Sequence 13, Appli
31	184	11.4	1634	1	US-07-816-283-1	Sequence 1, Appli
32	184	11.4	1634	2	US-08-417-103-1	Sequence 1, Appli
33	161.6	10.0	1518	1	US-08-148-215A-3	Sequence 3, Appli
34	149	9.3	1054	1	US-08-148-215A-1	Sequence 1, Appli
35	141.4	8.8	1296	1	US-07-816-283-9	Sequence 9, Appli
36	141.4	8.8	1296	2	US-08-417-103-9	Sequence 9, Appli
37	115	7.1	1796	1	US-07-816-283-11	Sequence 11, Appli
38	115	7.1	1796	2	US-08-417-103-11	Sequence 11, Appli
39	102.6	6.4	678	1	US-07-915-966C-3	Sequence 3, Appli
40	102.6	6.4	678	4	US-08-771-182-3	Sequence 3, Appli
41	102.6	6.4	678	5	US-08-853-194-3	Sequence 3, Appli
42	102.2	6.3	563	1	US-07-915-966C-2	Sequence 2, Appli
43	102.2	6.3	563	4	US-08-771-182-2	Sequence 2, Appli
44	102.2	6.3	563	5	US-08-853-194-2	Sequence 2, Appli
45	97.2	6.0	1586	2	US-08-461-244-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-889-108-7
Sequence 7, Application US/08889108
Patent No. 6103492
GENERAL INFORMATION:
APPLICANT: Yu, Lei
TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,108
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-889-108-7
Query Match 100.0%; Score 1610; DB 5; Length 1610;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGGATGAGCCCTGTGACTAAGTGGAGGGCGCTATACGACAGAGAAATGTGAG 60

|||||
Db 1 CGGATGACCTCTGTAACACTAAGTGGGAGGGGCTATACGAGAGGAAATGAC 60
QY 61 ATGCTACGCTGCTGCTCCGCTGACGCTCTCTGTCTACAGCAGAGTGGTTCT 120
Db 61 ATGCTACGCTGCTGCTCCGCTGAGAGCTCTCTGTCTACAGCAGAGTGGTTCT 120
QY 121 GTAGAAACACAGAGCTGTGGGAGGGGAGGAAAGGAGGCGCTGAGGCGCTGGAACCC 180
Db 121 GTAGAAACACAGAGCTGTGGGAGGGGAGGAAAGGAGGCGCTGAGGCGCTGGAACCC 180
QY 181 GAAAGTCTCGTCTCTGCTGCTACCTGCAAGCGCTCCGCGCGGCTGAGTACAT 240
Db 181 GAAAGTCTCGTCTCTGCTGCTACCTGCAAGCGCTCCGCGCGGCTGAGTACAT 240
QY 241 GGACAGCAGCGCTGCCCCCAGAACGCCAGCAATTCAGTATGCTTGGCTACTCAAG 300
Db 241 GGACAGCAGCGCTGCCCCCAGAACGCCAGCAATTCAGTATGCTTGGCTACTCAAG 300
QY 301 TTGCTCCCGACAGCCAGCCCGGCTCTGGGTCAACTTGTCCCACTTAAAGTGAACCT 360
Db 301 TTGCTCCCGACAGCCAGCCCGGCTCTGGGTCAACTTGTCCCACTTAAAGTGAACCT 360
QY 361 GTCCGACCCATGCGGTCCGAAACCGCACCCGACCTGGGCGGAGAGACAGCTGTGCTCC 420
Db 361 GTCCGACCCATGCGGTCCGAAACCGCACCCGACCTGGGCGGAGAGACAGCTGTGCTCC 420
QY 421 GACCGGAGTCTCTTCATGATCAGGCGCATCAGATCATGCGCTCTACTCATGCTG 480
Db 421 GACCGGAGTCTCTTCATGATCAGGCGCATCAGATCATGCGCTCTACTCATGCTG 480
QY 481 CGTGGTGGGCTCTTGGAACTTCTGCTGATGATGATGATGATGATGATGATGATGAT 540
Db 481 CGTGGTGGGCTCTTGGAACTTCTGCTGATGATGATGATGATGATGATGATGATGAT 540
QY 541 GAAGCTGCGCACCAACATCTACATTTTCACTTGTGCTGCGAGATGCTTAGCCACAG 600
Db 541 GAAGCTGCGCACCAACATCTACATTTTCACTTGTGCTGCGAGATGCTTAGCCACAG 600
QY 601 TACCGTCCCTTCCAGAGTGTGAATTAATGGAACATGCGCATTTGGAACATCCT 660
Db 601 TACCGTCCCTTCCAGAGTGTGAATTAATGGAACATGCGCATTTGGAACATCCT 660
QY 661 TTGCAAGATAGTATCTCATAGATTACTATACATGTTCAACAGCATATTCACCTCTG 720
Db 661 TTGCAAGATAGTATCTCATAGATTACTATACATGTTCAACAGCATATTCACCTCTG 720
QY 721 CACCATGAGTGTGATGATACATTTGAGTGTGCGACCTGTCAAGGCTTAGATTTCCG 780
Db 721 CACCATGAGTGTGATGATACATTTGAGTGTGCGACCTGTCAAGGCTTAGATTTCCG 780
QY 781 TACGCCCGGAAATGCAAAATTAATTAATGTGCAACTGAGTCCCTCTTCAAGCATGG 840
Db 781 TACGCCCGGAAATGCAAAATTAATTAATGTGCAACTGAGTCCCTCTTCAAGCATGG 840
QY 841 TCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 841 TCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 AACATTTCTCATCCCAACCTGGTACTGGGAAACCTGTGAGATCTGTGTTTATCTT 960
Db 901 AACATTTCTCATCCCAACCTGGTACTGGGAAACCTGTGAGATCTGTGTTTATCTT 960
QY 961 CGCCTTATATGCGAGTGTATATACGCTGTGCTATGAGTGTGAGTGTGAGTGTGAGT 1020
Db 961 CGCCTTATATGCGAGTGTATATACGCTGTGCTATGAGTGTGAGTGTGAGTGTGAGT 1020
QY 1021 CAAGAGTCTCGCATGCTCTGTGCTCCAAAGAAAGAGACAGAGATCTTGAAGATAC 1080
Db 1021 CAAGAGTCTCGCATGCTCTGTGCTCCAAAGAAAGAGACAGAGATCTTGAAGATAC 1080
QY 1081 CAGATGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1140
Db 1081 CAGATGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1140

Db 1081 CAGATGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1140
QY 1141 CGTATATTAACCTTTGTTAGTATCCAGAAACATACGTTCAGACTGTTTGTGCA 1200
Db 1141 CGTATATTAACCTTTGTTAGTATCCAGAAACATACGTTCAGACTGTTTGTGCA 1200
QY 1201 CTTGCTATGCTCTAGTATACAAACAGTGTGCTGCAACCGATCTTATGATTTCT 1260
Db 1201 CTTGCTATGCTCTAGTATACAAACAGTGTGCTGCAACCGATCTTATGATTTCT 1260
QY 1261 GGATGAAACCTTCAAGAGTCTCAGAGATTCTGATCCCAACCTTCCAAATGGA 1320
Db 1261 GGATGAAACCTTCAAGAGTCTCAGAGATTCTGATCCCAACCTTCCAAATGGA 1320
QY 1321 GCAACAAACCTTCAAGAGTCTCAGAGATTCTGATCCCAACCTTCCAAATGGA 1380
Db 1321 GCAACAAACCTTCAAGAGTCTCAGAGATTCTGATCCCAACCTTCCAAATGGA 1380
QY 1381 AGTGATAGACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1381 AGTGATAGACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 ACAGGCTCTCATGCTATTCGACCTTCAACAGCTTAGAACCAACATGATGGAAGC 1500
Db 1441 ACAGGCTCTCATGCTATTCGACCTTCAACAGCTTAGAACCAACATGATGGAAGC 1500
QY 1501 AGTGGTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Db 1501 AGTGGTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1561 CATCAACCTTCTCTCTGCTGCGACCTGCTGCAACATTAAGGCGG 1610
Db 1561 CATCAACCTTCTCTCTGCTGCGACCTGCTGCAACATTAAGGCGG 1610

RESULT 2
PCT-US94-10358-7
Sequence 7, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT: MC OPIOID RECEPTORS: COMPOSITIONS AND METHODS
TITLE OF INVENTION: 17
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120.601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1610 base pairs
type: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 PCT-US94-10358-7

Query Match 100.0%; Score 1610; DB 6; Length 1610;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGATGACCTCTGTGAAGTGTGGAGGGGCTATACGACGAGAGAAATGTGAG 60
 DB 1 CGGATGACCTCTGTGAAGTGTGGAGGGGCTATACGACGAGAGAAATGTGAG 60
 QY 61 ATGCTACCTGCTGCTCCCTCCGCTGAGCTCTCTGTCTCAGCCAGAGATGTTCT 120
 DB 61 ATGCTACCTGCTGCTCCCTCCGCTGAGCTCTCTGTCTCAGCCAGAGATGTTCT 120
 QY 121 GTAGAAACAGAGAGAGTGTGGAGGGGCGAAAGAGCGGCTGAGGCGTTGGAAGCC 180
 DB 121 GTAGAAACAGAGAGAGTGTGGAGGGGCGAAAGAGCGGCTGAGGCGTTGGAAGCC 180
 QY 181 GAAAGTCTCGGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 181 GAAAGTCTCGGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 241 GGACAGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 241 GGACAGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 QY 301 TTGCTCCCGACAGACCGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 301 TTGCTCCCGACAGACCGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 361 GTCCGACCCATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 361 GTCCGACCCATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 421 GACCGGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 DB 421 GACCGGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 481 CGTGTGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 DB 481 CGTGTGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 541 GAAGACTGCGCAACAATCTACATTTTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 DB 541 GAAGACTGCGCAACAATCTACATTTTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 601 TACCTGCTTCCAGAGTGTGAATTTACCTAATGGGAACATGCGCATTTTGAACCATCTCT 660
 DB 601 TACCTGCTTCCAGAGTGTGAATTTACCTAATGGGAACATGCGCATTTTGAACCATCTCT 660
 QY 661 TTGCAAGATGATGATCTCATAGATTACTATACATGTTCCACCAATATTCACCTCTG 720
 DB 661 TTGCAAGATGATGATCTCATAGATTACTATACATGTTCCACCAATATTCACCTCTG 720
 QY 721 CACCATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 DB 721 CACCATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 QY 781 TACCTGCTTCCAGAGTGTGAATTTACCTAATGGGAACATGCGCATTTTGAACCATCTCT 840
 DB 781 TACCTGCTTCCAGAGTGTGAATTTACCTAATGGGAACATGCGCATTTTGAACCATCTCT 840
 QY 841 TCTTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 DB 841 TCTTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 QY 901 AACATTTCTCATCCACCTGTGAGTGGGAAACCTGCTGGAAGATCTGTGTTTATCTT 960
 DB 901 AACATTTCTCATCCACCTGTGAGTGGGAAACCTGCTGGAAGATCTGTGTTTATCTT 960

QY 961 CGCCTTCAATATGCGACAGTCTCATCATTTACCGTGTGCTATGAGATGATGATCTTGCGCT 1020
 DB 961 CGCCTTCAATATGCGACAGTCTCATCATTTACCGTGTGCTATGAGATGATGATCTTGCGCT 1020
 QY 1021 CAAGAGTGTGCGCAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 DB 1021 CAAGAGTGTGCGCAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 QY 1081 CAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 DB 1081 CAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 QY 1141 CGTATCATTTAAGCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 DB 1141 CGTATCATTTAAGCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 QY 1201 CTTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
 DB 1201 CTTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
 QY 1261 GGATGAAACCTTCAAAACGATGCTTCAAGAGTCTGTAATCCAACTCTTCCAACTTGA 1320
 DB 1261 GGATGAAACCTTCAAAACGATGCTTCAAGAGTCTGTAATCCAACTCTTCCAACTTGA 1320
 QY 1321 GCAACAAACCTTCAAAACGATGCTTCAAGAGTCTGTAATCCAACTCTTCCAACTTGA 1380
 DB 1321 GCAACAAACCTTCAAAACGATGCTTCAAGAGTCTGTAATCCAACTCTTCCAACTTGA 1380
 QY 1381 AGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 DB 1381 AGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 QY 1441 ACAGGCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 DB 1441 ACAGGCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 QY 1501 AGGTTGCTTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
 DB 1501 AGGTTGCTTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
 QY 1561 CATCCAACTCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1610
 DB 1561 CATCCAACTCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1610

RESULT 3
 US-08-889-108-1
 : Sequence 1, Application US/08889108
 : Patent No. 6103492
 : GENERAL INFORMATION:
 : APPLICANT: Yu, Lei
 : TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
 : NUMBER OF SEQUENCES: 17
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Arnold, White & Durkee
 : STREET: P. O. Box 4433
 : CITY: Houston
 : STATE: TX
 : COUNTRY: USA
 : ZIP: 77210-4433
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/889,108
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/305,518
 : FILING DATE:


```

RESULT      5
PCT-US94-10358-1
; Sequence 1, Application PC/TUS9410358
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10358
; FILING DATE: Concurrently herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120,601
; FILING DATE: 13 SEPTEMBER 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDIA00SP--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; Telex: 79-0924
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 214..1410
; PCT-US94-10358-1

Query Match          69.8%; Score 1123.8; DB 6; Length 1618;
Best Local Similarity 83.7%; Pred. No. 7.9e-291;
Matches 1323; Conservative 0; Mismatches 247; Indels 11; Gaps
    4.

QY   27 GTGGGAGGGGGCGTATACGAGAGAAGAAATGCAGATGTCAGTGCGGTCCGCCGCCG 86
Db   2  GTGGGAAGGGGGGTACTACAGAGAGAGAAATAATCAGACGCTCAAG-CGTTCCCTTCTGCTG 60
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   87 ACGCTCTCTCTGTGTCACACCAGAGCATGCTTTCTGTAAAGAACAGCAGAGG-CTGTGGA 145
Db   61 CGCGCTCTCTCGTGGTTCCACTAGAGGGGTGGTTCATGTAAAGATTGACGAGAGCTAAGGA 120
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   146 GCGGCGAAAGAGAGCGGCTGTAGGCGCTTGGAAACCCGAAAAAGTCTGGGCTCTCTGGCTAC 205
Db   121 GCTGTGAGAGGAGAGGCGTGGGGCGCGTAGAACCCGAAAAGTCTGTAGTCTCTCACTAC 180
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   206 CTGCGACAGCGCGCCCCCGGCCGCGCAATACATGAGAGACAAGACGCGTCCCACCAGAAC 265
Db   191 AGCTTAAGCTAGTCGACAGAGAGCGCTTTCACACCATGAGAGACGACGCGGACCGAGGAAC 240
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   266 GCCACCAATTTGACATGATGCTTTGGCGTACTCAAGTTGCTCCACAGACCAGCCCGGT 325
Db   241 ACCACAGCATGTGTCAGACCCCTTAGCTACAGGCAAGTTGCTCCACACA-----CGTGGC 294
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   326 TCTCTGGTTCACATTGTCACATTAGATGGCAACTGTCTCGACCCATGCGGTCCGAACCGC 385

```

Db	235	TCCTGGCTCAACTGTGTCCACGCTGATGTGGCAACAGTCCGATCCATGGGGTCTGAACGC	354
Qy	386	ACCGACCTGGGGCGGAGAGACAGCCTGTGCGCTCCGACCGGAGTCCCTCATGTATCAG	445
Db	355	ACCGGGCTTGGCGGGAACGACACCTGTCCCTCCACAGACCGGACGCCCTTCATGGTTCACA	414
Qy	446	GCATTCACGACATAGGCGCCCTCTACTCCATCCATCGTGTGGTGGGGCCCTTGGGAAACTTC	505
Db	415	GCATTTTACATCAATGGCGCCCTTACTCTATCTGTGTGTGTGTGTGTGGGAGCACTTC	474
Qy	506	CTGGTCACTGATGTGATGTTCAGATATACACCAAGATGAAGACTGCCACCAACATCTACATY	565
Db	475	CTGGTCACTGATGTGATGT	534
Qy	566	TTCAACCTTGTCTGTGGAGATGCTTATAGCCACAGTACCTTGCCTTCCAGATGTGAT	625
Db	535	TTCAACCTTGTCTGTGGAGAGCGCCTTAGCGACAGTACCTGCCCTTACAGATGTCAAC	594
Qy	626	TACCTATGGGAACATGGCCATTTTGGAAACCATCTTTGGAATATGTATCTCCATATAT	685
Db	595	TACCTGTATGGGAACATGGCCCTTGGAAACCATCTTGTGAATATGTATCTCCATATAT	654
Qy	686	TACTATTAACATGTTCACACAGCATATTACCCCTCTGCACATGAGTGTGATCATACTY	745
Db	655	TACTATTAACATGTTCACACAGCATATTACCCCTCTGCACATGAGTGTGATCATACTY	714
Qy	746	GCACTGTGCCACCCCTGTCAAGGCGCTTAGATTTCCGTACTCCCGGAATGCCAAATTTATC	805
Db	715	GCTGTGTGCCACCCAGTCAAGGCGCTTAGATTTCCGTACTCCCGGAATGCCAAATTTATC	774
Qy	806	AATGTCTGCAACATGTGAAATCCCTCTTACAGCATTTGGCTTCCCTGTATGTATAGGCTACA	865
Db	775	AAGTCTGTGCAACATGTGAAATCCCTCTTACAGCATTTGGCTTCCCTGTATGTATAGGCAACC	834
Qy	866	ACAAATAATACAGCAAGGTGCTCAGATAGTTTACACTATTAATTTCTCATCAACACGTGTAC	925
Db	835	ACAAATAATACAGCAAGGTGCTCAGATAGTTTACACTATTAATTTCTCATCAACACGTGTAC	894
Qy	926	TGGGAAAACCTGTGAAGATCTGTGTTTTCATCTTCCCTTCAATTATGCCATGCTCATC	985
Db	895	TGGGAAAACCTGTGAAGATCTGTGTTTTCATCTTCCCTTCAATTATGCCATGCTCATC	954
Qy	986	ATTACCGTGTGCTATGTGATGATGATCTTGGCGCTCAGAAGTGTCCGATGTCTCTGTGC	1045
Db	955	ATTCAGTGTGTGATGATGATGATGATCTTGGCGCTCAGAAGTGTCCGATGTCTCTGTGC	1014
Qy	1046	TCCAAAGAAAAGGACAGGAATCTTCGAAGATACACAGATGTGCTGGTGTGTGCT	1105
Db	1015	TCCAAAGAAAAGGACAGGAATCTTCGAAGATACACAGATGTGCTGGTGTGTGCT	1074
Qy	1106	GTGTTCATCGT	1165
Db	1075	GTATTTATTCGT	1134
Qy	1166	ATCCCAAGAAACTACGTCTCAGACTGTTTCTTGGACATTTGCATTTGCTGTAGTTACACA	1225
Db	1135	ATTCCAAGAAACTACGTCTCAGACTGTTTCTTGGACATTTGCATTTGCTGTAGTTACACG	1194
Qy	1226	AACGCTGCCCTCAACCCAGTCTTTATGTGATTTCTGGAATGAAGAACTTCAAGCATGCTC	1285
Db	1195	AACGCTGCCCTCAACCCAGTCTTTATGTGATTTCTGGAATGAAGAACTTCAAGCATGCTC	1254
Qy	1286	AGAGATTTCTGTATCCCAACCTCTTCAACATGTGAGCAACAACCTCACTGTGATTTGT	1345
Db	1255	AGAGATTTCTGTATCCCAACCTCTCTCAACATGTGAGCAACAACCTCACTGTGATTTGT	1314
Qy	1346	CAGAAGACTAGAGACCAACCCCTCAGGGCAATATACAGTGTGATGAACTAATCATACGTA	1405
Db	1315	CAGAAGACTAGAGAGCAATCCCTCAGGGCAATATACAGTGTGATGAACTAATCATACGTA	1374
Qy	1406	GAATATCTGGAGCAGAACTGCTCCGTTCCTTAACAGGGTCTCATGCAATTCGACACT	1465

Db 1375 GAAATCTGAGAGGAAACTGCTCATTTGCCCTAAGTGGCTCAGACATCCAGACC 1434

QY 1466 TCACCAAGCTTAGAAGCCACCATGTATGTGAGAGAGTGGCTTCACAAATGTAGAG 1525

Db 1435 TCGTAGAGCTTAGAGGCGCGCTACGTGAGATCAGGTCTGTGAGGGTGTGGAG 1494

QY 1526 GCTTAATCTCTAGAAAGTGGCTTTAGTGCATCACAACCTTTCTCTGCGCC 1585

Db 1495 GCTGTGGTTCTCTGAGAAA---CCATCTGATCTGTCATTCAAAAGTCAATTCCTCTGCT 1551

QY 1586 ACTCTGCTCTGACATTTAGAG 1606

Db 1552 ACTTCACTCTGACATGAGAG 1572

RESULT 6

PCT-US94-10358-3

Sequence 3, Application PC/TUS9410358

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P. O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/10358

FILING DATE: Concurrently herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/120,601

FILING DATE: 13 SEPTEMBER 1993

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARK B.

REGISTRATION NUMBER: 37,259

REFERENCE/DOCKET NUMBER: INDA005P--

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679

TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1618 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 339..1235

PCT-US94-10358-3

Query Match 69.8%; Score 1123.8; DB 6; Length 1618;

Best Local Similarity 83.7%; Pred. No. 7.9e-291;

Matches 1323; Conservative 0; Mismatches 247; Indels 11; Gaps 4;

QY 27 GTGGAGAGGGGCTATACGAGAGAGATGTCAGATGCTCAGTCCGCTCCGCTG 86

Db 2 GTGGAGAGGGGCTCAAGAGAGAGAGATATACAGCTCAGA-CGTTCCCTTTCGCTG 60

QY 87 ACAGCTCTCTCTGTCTAGCCAGAGCTGTTCTGTAGAAAACAGCAGAG-CGTGGCA 145

Db 61 CCGCTCTCTCTGTCTAGCCAGAGCTGTTCTGTAGAAAACAGCAGAG-CGTGGCA 120

QY 146 GCGGCAAGAGAGCGGCTGAGGGCTTGGAAACCCGAAAGTCTCGTGTCTGCTAC 205

Db 121 GCTGTAGAGAGAGAGAGCTGGGGCGCTGGAGACCCGAAAGTCTGAGTCTAGTTAC 100

QY 206 CTCGCACAGCGTGGCCGCGCGCGCTGAGTACATGAGACAGACGCTGCCCGCAGCAAC 245

Db 181 AGCCTACCTAGTCCGACAGAGGCTTCAAGACCATGAGACAGACCGCGCCAGGGAG 247

QY 266 GCCAGCAATTGCTACTGATGCCCTTGGCTACTCAAGTTGCTCCGAGCAACCGCCGCT 325

Db 241 ACCAGCGAGCTGCTCAGACCCCTTAGCTCAGGCAAGTGTCTCCAGCA-----CTGGGC 294

QY 326 TCTGGGCTCAACTGTTCCCACTTATGATGGCAAGCTGTCCAGCCATCGGTCCAGCCG 385

Db 295 TCTGGGCTCAACTGTTCCCACTTATGATGGCAAGCTGTCCAGCCATCGGTCCAGCCG 354

QY 386 ACCGAGCTGGGCGGAGAGAGAGCTGGCGCTCGAGCCGAGCTCCCTCATGATCAGC 445

Db 355 ACCGAGCTGGGCGGAGAGAGAGCTGGCGCTCGAGCCGAGCTCCCTCATGATCAGC 414

QY 446 GCCATCAGATCATGGCCCTCTACTCATGCTGTGCGTGGGCTCTTGGAACTTC 505

Db 415 GCCATTCAGATCATGGCCCTCTACTCATGCTGTGAGTGGGCTCTTGGAACTTC 474

QY 506 CTGCTCATGATGATGATTTGATGATACACCAAGATGAAGCTGCCACCAATCTACAT 565

Db 475 CTGCTCATGATGATGATTTGATGATACACCAAGATGAAGCTGCCACCAATCTACAT 534

QY 566 TTCAACCTTGGCTGGGAGATGCTTGGAGCAGCTGACCTGCTCCAGAGTGTAT 625

Db 535 TTCAACCTTGGCTGGGAGATGCTTGGAGCAGCTGACCTGCTCCAGAGTGTAT 594

QY 626 TACCTAATGGAGACATGGCCATTTGGAACATCTTGGCAAGATGATCTCCATGAT 685

Db 595 TACCTAATGGAGACATGGCCATTTGGAACATCTTGGCAAGATGATCTCCATGAT 654

QY 686 TACTATTAACATGTTCCACAGATATTACCCCTCGACACCATGATGTTGATCATATT 745

Db 655 TACTATTAACATGTTCCACAGATATTACCCCTCGACACCATGATGTTGATCATATT 714

QY 746 GCAGTGGCAACCTGTCAGAGCTTATGATTTCCGTAAGTCCCGCAATATGCAATATC 805

Db 715 GCTGTCTGCAACCTGTCAGAGCTTATGATTTCCGTAAGTCCCGCAATATGCAATATC 774

QY 806 AATGCTGCAACCTGATCTCTCTTCAAGCATGCTTCTGTAATGTTGATGCTAC 865

Db 775 AATGCTGCAACCTGATCTCTCTTCAAGCATGCTTCTGTAATGTTGATGCTAC 834

QY 866 ACAAAATACAGGCAAGTTCATGATTTGATACATACATTTCTCATCCAGCTGTAC 925

Db 835 ACAAAATACAGGCAAGTTCATGATTTGATACATACATTTCTCATCCAGCTGTAC 894

QY 926 TGGGAAACCTGCTGAGATGCTGTTTCATCTGCTGCTTATGAGCAGTGTATC 985

Db 895 TGGGAAACCTGCTGAGATGCTGTTTCATCTGCTGCTTATGAGCAGTGTATC 954

QY 986 ATACGCTGTCTATGAGCATGATGATCTTGGCTCAAGAGTCCGATGCTCTGCGC 1045

Db 955 ATACGCTGTCTATGAGCATGATGATCTTGGCTCAAGAGTCCGATGCTCTGCGC 1014

QY 1046 TCCAAAAGAAAGAGCAGGATCTTCAAGATACACAGATGCTGTGTGTGTGCT 1105

Db 1015 TCCAAAAGAAAGAGCAGGATCTTCAAGATACACAGATGCTGTGTGTGTGCT 1074

QY 1106 GTGTTATGCTGTGCTGAGTCCATTCATTTAGTCTGATTAAGGCTTGGTATCA 1165

Db 1075 GTATTTATGCTGTGCTGAGTCCATTCATTTAGTCTGATTAAGGCTTGGTATCA 1134

QY 1166 ATCCAGAAATACAGTTCAGAGCTTCTTGGCACTTGTGATTTGCTAGTTACCA 1225

Db 1135 ATCCAGAAATACAGTTCAGAGCTTCTTGGCACTTGTGATTTGCTAGTTACCA 1194

Oy	1226	AACGCGCCCTCAACCAGGCTCTTATGATTCCTGATGAACCTC	1285
Dd	1195	AACGCTGCTGAAATCCAGTTCTTTACGCTTCTTGATGAACCTC	1284
Oy	1286	AGAGAGTTCTGTATCCCAACCTCTTCCAACTTGAACAACAACTC	1345
Dd	1255	AGAGAGTTCTGTATCCCAACCTCTGTCAGATGGAACAACAACTC	1314
Oy	1346	CAGAACCTAGAACCCACCCCTCCAGGGCCATACAGTGATGAACT	1405
Dd	1315	CAGAACCTAGGGAACATCCCTCCAGGGCTAAATACGTGATGAACT	1374
Oy	1406	GAAATCTGGAAGACAGAAATCGCTCCGTTGCCCTACAGGGTCTAT	1465
Dd	1375	GAAATCTGGAAGGACGAAATCGCTCCATTCCTTAACCTGGTCTAC	1434
Oy	1466	TCACCAAGCTTAGAAGCCACCATGATGTGGAAGCAGGTGGTTC	1525
Dd	1435	TCGCTAGCTTAGAGGCGCCGACATCTACGTGAAATCAGTTGCTG	1494
Oy	1526	GCTCTAATCTCTAGAAATGCTGCTTTTAAAGTATCCAACTCTTT	1585
Dd	1495	GCTCTGTTTCCGTGAGAA---CCATCTGATCTCGATTCAAAGTCAT	1551
Oy	1586	ACTCTGCTGCACATATAGAG	1606
Dd	1552	ACTTCACTCTGCACATAGAG	1572

RESULT 7
US-08-411-859-1

; GENERAL INFORMATION:

APPLICANT: KEITH JR., DUANE E.

TITLE OF INVENTION: EXPRESSION CLONING OF A DELTA OPIOID

TITLE OF INVENTION: PHARMACEUTICALS

CORRESPONDENCE ADDRESS:

STREET: 755 Page Mill Road

STATE: California

ZIP: 94304-1018

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

```

; CURRENT APPLICATION DATA:
; ADDITION MONTH: 03/00/411 0500

```

FILING DATE:

PRIOR APPLICATION DATA: TFC 07/0330 3000
ADDITIONAL WHEED: TFC 07/0330 3000
;

FILING DATE: 13-AUG-1999

NAME: LITHGOW, TIMOTHY J
REGISTRATION NUMBER: 36

REFERENCE/DOCKET NUMBER: 22000-20526.00

TELEPHONE: 415-813-56
TELEFAX: 415-404-0703

TELEX: 706141
INFORMATION FOR SEO ID NO. 3

SEQUENCE CHARACTERISTICS:

TYPE: nucleic acid

```

; TOPOLOGY: linear
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 29..1144
;
US-08-411-859-1

```

Query Match	27.58	Score 443.2	DB 4	Length 1829
Best Local Similarity	67.38	Pred. No. 4.1e-109		
Matches 641	Conservative 0	Mismatches 308	Indels 3	Gaps 1

OY	432	CCTCATGATCAGCGCCATCACATCATATGGCCCTCTACTACCTCATCTGTCGGTGGGGGC	491
Db	159	CGTCCCTGGCCATAGCCATGCGCATACCGCGCGTCTACTCGGCTGTGTGGCGATGGGGC	218
OY	492	TCTTGGAAACTTCCTGCTGATGTATGTATGTCTAGATATACCAAGATGAAGACTGCCA	551
Db	219	TTCTGGGCAACTGCTGCTGATTTGGATCGTCCGGTACCAAAATTTTGAAGACCCCA	278
OY	552	CCAACTCTCACTTTCAACCTTGCCTGTGGAGATGCCCTTACCACACAGTACCCCGGCT	611
Db	279	CCAACTCTCACTTTCAACTTGGCTTTGGCTGTATGCGTGGCCACACAGACGCTGCCCT	338
OY	612	TCCAGATGTGAATTACTCTATGGGAACATGGCCATTGGAACTATCCCTTTGCAAGATAG	671
Db	339	TCCAGAGCCGCCAGTACTTATGTGAAACAGTGGCCGCTTGGCAGAGCTGCTGTCAAGCTG	398
OY	672	TGATCTCCATAGATTACTATATACATGTTCACGACATATTCACCCCTGTGCACCATGAGTG	731
Db	399	TGCTCTCCATGTACTACTACACATGTTCACATGTTCACCTTCACACATGATATGAGCG	458
OY	732	TTGATGCATTCATTCAGAGTGTGCACCCGTGCAAGGCCCTTAATTTCCGTAATCCCCGA	791
Db	459	TGGACCCCTATATTGCTGTGTGCATCTGTCAAAACCCCTGGACTCTCGGACACGCA	518
OY	792	ATGCCAAATATTAATGATGTGTGCACATGATCCCTCTTCCACCATTTGGTCTTCCTGTAA	851
Db	519	AGGCCAAGCTGTATCAATATATGCACTGTGGGTCTTGGCTTCAGGTGTGGGGTCCCATCA	578
OY	852	TGTTTCATGCGTACCACAAAATACAGGCAAGTTCCATAGATTGTACTACATCAATCTCTC	911
Db	579	TGCTCATGCGAGTACCCCAACCCCGGAGTGTGCATAGTATGCACTGCCAGTTCCCA	638
OY	912	ATCCAACTGTACTGGGAAACCTGCTGAATCTGTGTTTCAATCTTCCGCTTCATTA	971
Db	639	GTCCCACTGTACTGGGACATGTCACCAAGATCTGCTCTTCCCTTTGGCTTCTGGG	698
OY	972	TGCCAGTGTCAATCATTACCGTGTGCTATGAGATGATATCTTGGCCCTCAAGATGTGC	1031
Db	699	TGCCGATCTCTCATCATCAGGTTGCTGTATGGCTCTACTGTACTGGCCCTGGCGACAGCTGC	758
OY	1032	GCATGCTCTCTGGCTCCMAAGAAAGAGACAGGATTTTGAAGATACACAGAGTGTGC	1091
Db	759	GTCTGTCTCGGGTTCCAAGAGAGAGACCGCAGCGCTGGGGGACACCGGCATGTGTC	818
OY	1092	TGTGTGTGTGTGCTGTGTATGTCTGCTGCACTCCATTACATTTACGTCAATTA	1151
Db	819	TGTGTGTGTGTGGGGGCTTCTGTGTGTGTGTGGGGCCCATCCACATCTTTCGTCATGTCT	878
OY	1152	AAGCTTTGTATTAATC--CCAGAAATACGTTCCAGACGTTTCTTGGCACCTTGTCA	1208
Db	879	GGACGCTGTGTGACATTAATCGCGGAGACCCACTTGTGTGTGGCCGCACTGCACCTGTGCA	938
OY	1209	TTGCTTAGGTACACAAACAGCTGCTCCTCAACCCAGTCTTTATGCATTTCTGTGATGAA	1268
Db	939	TTTGGCTGTGGGCTAGCGCAACAGCAGCTCAACCCGGTTCTAGACGCTTCTCGACGAGGA	998
OY	1269	ACTTCAAAAGATGCTTCAGAGAGTTCTGTATCCCAACTCTTCAACAATTGACAACTAA	1328
Db	999	ACTTCAAGCGCTGTTCCGCAAGCTCTGTGCGACGCGCTGCGGCGCCAAAGAACCGGCA	1058
OY	1329	ACTGCATCTGATTTCTGACAGAACTAGAGACACCCCTCCACGGCGCAATAC	1380

Db 1059 GTCTCGTCGTCGCCGCCAGCCACGCGTGTGAGGTGTCACTGCTGCAC 1110

RESULT 8

US-08-147-592A-3

Sequence 3, Application US/08147592A

Patent No. 6096513

GENERAL INFORMATION:

APPLICANT: Bell, Graeme I

APPLICANT: Reisine, Terry

APPLICANT: Yasuda, Kazuki

TITLE OF INVENTION: Opioid Receptor Genes,

TITLE OF INVENTION: Compositions and Methods

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: United States of America

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/147, 592A

FILING DATE: 05-NOV-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/100, 694

FILING DATE: 30-JUL-1993

CLASSIFICATION: 435

APPLICATION NUMBER: 08/066, 296

FILING DATE: 20-MAY-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Wilson, Mark B.

REGISTRATION NUMBER: 37,259

REFERENCE/DOCKET NUMBER: ARCD:105

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

TELEX: N/A

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2272 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 12..1127

US-08-147-592A-3

Query Match 27.5%; Score 443.2; DB 5; Length 2272;

Best Local Similarity 67.3%; Pred. No. 4.5e-109;

Matches 641; Conservative 0; Mismatches 308; Indels 3; Gaps 1;

QY 432 CCTCATATATACGCGCATACAGATATGCGCTTACTCCATCGTGTGCGTGGGCG 491
DB 142 GCTCCCTGCGCTTACGCGCATACGCGCTTACTCGGCTGTGCGAGTGGGCG 201
QY 492 TCTTGAAGAACTTCTGCGATGTATGTATGTAGATACCAAGATGAGACTGCCA 551
DB 202 TTCTGGGCAAGTGTGCTGTATGTATGTATGTATGTATGTATGTATGTATGTAT 261
QY 552 CCAACATCTACATTTTCAACCTTGTCTGTGAGATGCGCTTACCAACGATCCCTG 611
DB 262 CCAACATCTACATTTTCAACCTTGTCTGTGAGATGCGCTTACCAACGATCCCTG 321

QY 612 TCCAGATGTGATTAACCTAATGGAAATGCGCATTTTGAAACATTCCTTTGACAGATAG 671

DB 322 TCCAGAGCGCCAGATCTGATGAGAAAGCTGTGGCGAGCTGTGCAAGGCTG 381

QY 672 TGATCTCCATAGATTAACATATACATGTTCACGAGATATTCACCTCTGACCATAGATG 731

DB 382 TGCTCTCCATGATTAACATATACATGTTCACGAGATATTCACCTCTGACCATAGATG 441

QY 732 TTGATGATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 791

DB 442 TGACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 501

QY 792 ATGCCAAATTAATCAATGTGTGCAATGATGATGATGATGATGATGATGATGATG 851

DB 502 AGGCCAAATTAATCAATGTGTGCAATGATGATGATGATGATGATGATGATGATG 561

QY 852 TGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 911

DB 562 TGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 621

QY 912 ATCAACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 971

DB 622 TGCCAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 681

QY 972 TGCCAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1031

DB 682 TGCCAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 741

QY 1032 GCATCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1091

DB 742 GTCTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 801

QY 1092 TGCTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1151

DB 802 TGCTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 861

QY 1152 AAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1208

DB 862 GACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 921

QY 1209 TTGCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1268

DB 922 TTGCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 981

QY 1269 ACTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1328

DB 982 ACTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1041

QY 1329 ACTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380

DB 1042 GTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1093

RESULT 9

US-08-147-592A-1

Sequence 1, Application US/08147592A

Patent No. 6096513

GENERAL INFORMATION:

APPLICANT: Bell, Graeme I

APPLICANT: Reisine, Terry

APPLICANT: Yasuda, Kazuki

TITLE OF INVENTION: Opioid Receptor Genes,

TITLE OF INVENTION: Compositions and Methods

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: United States of America

ZIP: 77210

COMPUTER READABLE FORM:

Db 918 GAGGAGAGACCGAAACCTGCGGGGTATCATCGACTGCTGTGTAGTGTGGCTGTGT 977
QY 1110 TCATCTCTCTCTGAGTCCCATTCACATTTAGTCATCATTAAGCTTGGTACATCC 1169
Db 978 TTGTGGCTCTGCTGAGCCGCTGCTGCTGTCTGTCTGCTGCTGCTGCTGCTGCTG 1037
QY 1170 CAGAACTACCTGCTGAGACTGTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1229
Db 1038 CAGGTAGTGAAGTGCAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1097
QY 1230 GCTGCTCAACCCAGTCTTTATGATTTCTGATGATGATGATGATGATGATGATGATG 1289
Db 1098 GTTGTCTCAATGCTATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1157
QY 1290 AGTTCTGTATCCCAAGCTCTTCCACATTTAGACAAACAACTGCTGCTGCTGCTG 1344
Db 1158 AGTTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1212

RESULT 13
US-08-454-549-1
; Sequence 1, Application US/08454549
; Patent No. 5866324
; GENERAL INFORMATION:
; APPLICANT: EPPLE, C. Mark
; APPLICANT: OZENBERGER, Bradley A.
; APPLICANT: HUMES, Jeffrey D.
; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,549
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1A818-US5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2706 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
TISSUE TYPE: Rat brain
US-08-454-549-1

Query Match 22.6%; Score 363.8; DB 3; Length 2706;
Best Local Similarity 62.9%; Pred. No. 7.7e-88;
Matches 563; Conservative 0; Mismatches 332; Indels 0; Gaps 0;

QY 450 TCACGATCATGCCCTCTACTCATCTGTGCTGTGGGCTCTTGGAACTTCTCTGG 509
Db 252 TCACGATCATGCCCTCTACTCATCTGTGCTGTGGGCTCTTGGAACTTCTCTGG 311

QY 510 TCATGATGATGATTCAGATATACCAAGATGAAGACTGCCACCAATCATTTTCA 569
Db 312 TCATGATGATGATTCAGATATACCAAGATGAAGACTGCCACCAATCATTTTCA 371
QY 570 ACCCTCTCTGAGAGATGCTTGAAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 629
Db 372 ATCTGACATGCTGATATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 431
QY 630 TAATGGAAATGCTGCTTGAAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 689
Db 432 TACTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 491
QY 690 ATACATGTTTCAACAGATATATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 749
Db 492 ACACATGTTTCAACAGATATATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 551
QY 750 TCTGCCACCTGCTGAGGCTTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 809
Db 552 TCTGCCACCTGCTGAGGCTTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 611
QY 810 TCTGCCACCTGCTGAGGCTTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 869
Db 612 TCTGCCACCTGCTGAGGCTTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 671
QY 870 ATACAGGAGGCTTCAATGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 929
Db 672 AATGAGAGGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 731
QY 930 AATGAGAGGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 989
Db 732 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 791
QY 990 CCGTGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1049
Db 792 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 851
QY 1050 AAGAAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1109
Db 852 GAGGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 911
QY 1110 TCATCTCTCTCTGAGTCCCATTCACATTTAGTCATCATTAAGCTTGGTACATCC 1169
Db 912 TTGTGGCTCTGCTGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 971
QY 1170 CAGAACTACCTGCTGAGACTGTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1229
Db 972 CAGGTAGTGAAGTGCAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1031
QY 1230 GCTGCTCAACCCAGTCTTTATGATTTCTGATGATGATGATGATGATGATGATGATGATG 1289
Db 1032 GTTGTCTCAATGCTATCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1091
QY 1290 AGTTCTGTATCCCAAGCTCTTCCACATTTAGACAAACAACTGCTGCTGCTGCTG 1344
Db 1092 AGTTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1146

RESULT 14
US-08-454-552-1
; Sequence 1, Application US/08454552
; Patent No. 6005072
; GENERAL INFORMATION:
; APPLICANT: EPPLE, C. Mark
; APPLICANT: OZENBERGER, Bradley A.
; APPLICANT: HUMES, Jeffrey D.
; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue
; CITY: New York

```

STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,552
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1A818-USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
TELEX: 236687
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2706 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE: Rat brain
TISSE TYPE: Rat brain
US-08-454-552-1

```

Query Match 22.6%; Score 363.8; DB 5; Length 2706;

Best Local Similarity 62.9%; Pred. No. 7.7e-88; Matches 553; Conservative 0; Mismatches 332; Indels 0; Gaps 0;

```

450 TCACGATCATGCGCTCTACTCCATCGTGTGCGTGGGCTCTTCGAACTCTCTGG 509
252 TCACCATCGTGGGCTCTACTTGGCTGTGTGATCGGCGGCTCTCGGGAACGCTCG 311
510 TCATGTATGTGATGTTCAGTATACCAAGATGAAGACTGGCACCACATCTTATTTCA 569
312 TCATGTATGTGATGTTCAGTATACCAAGATGAAGACTGGCACCACATCTTATTTCA 371
570 ACCTTGCTGGGAGATGCTTAGCCACAGTACCTTCCGCTCCAGAGTGAATTAC 629
372 ATCTGGCAGCTGGTATACCTCTGTCTGTACACACTGCCCTTCCAGGACAGATCC 431
630 TAATGGGAACATGGCCATTTGGAACATCTTTCAGAGATAGTATCTCCATAGATTACT 689
432 TACTGGGCTCTGCGCATTTGGGAATGCACTGTGCAAGACTGTCAATGTATGACTACT 491
690 ATTAACATGTTCACACATTTTACCTCTGACACATGATGTGTGATTCATATTCGAG 749
492 ACAACATGTTTACACACACTTTTACCTGACCGCCATGAGCCGTAGTGTGCTA 551
750 TCGCCACCTGTCGAAGGCTTATTCGCTTCCGCTCCGCAAAATATATCATG 809
552 TCGCCACCTTATCCGCTGCTGATGTGTGACATTCAGCAAAAGCCAGCTTATATG 611
810 TGTGCAATGATGCTCTCTTTCAGCCATGCTTCTCTGTATATGTTTCAGGTACAA 869
612 TGGCCATATGAGGCGCTGAGTGTGTGCTCTGTGCAATCATGCTGTTACAGCAC 671
870 AATACAGGCAAGTTCATATGATTTACATATCTTCTATCCAACTGGTACTGGG 929
672 AAGTGAAGATGAAGATGAGTGTGCTGAGATCCCTGCGCTCAGAGACTATTTGG 731
930 AAAACCTGCTGAAGATCTGTGTTTTCATCTTCCCTTATATTCAGAGTCAATTA 989
732 GCCCTTATTTGCGCATCTGATCTTCTCTTTTTCCTTTCATCATCCCTGTCTATCATCT 791
990 CCGTGTGATGAGTATGATGATCTTGGCGCTCAAGAGTGTCCGATGCTCTGTGCTCCA 1049

```

```

DB 792 CTCTGTGCTACAGCCCTCATGATTCGACGACTTCGTGTGCTGCTTTCAGCTCC 851
1050 AAGAAAGGACAGGAATCTTCGAAGATCACAGATGTGTGTGTGTGTGTGTGT 1109
852 GGGAGAGAGCCAAACCTGCGGCTATCATCTGATGTGTGTGTGTGTGTGTGT 911
1110 TATCTGTGCTGAGTATCCATTCATATTAAGCTTGTGTGTGTGTGTGTGTGT 1169
912 TGTGTGCTGCTGAGACGCTGTGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 971
1170 CAGAACTACGTTCCAGACTGTTCTTGGCACTTCTGATGCTTACGTTACACAA 1229
972 CAGTGTGATGAGATGAGTGTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1031
1230 GCTGCTCAACCCAGTCTTATGATTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1289
1032 GTTGTCTCAATCCATCTCTATGCTTCTGTGTGTGTGTGTGTGTGTGTGTGT 1091
1290 AGTCTGTATCCCACTCTCTCCATGAGCAACAAACTCCACTGCAATTCG 1344
1092 AGTCTGTGCTGTGCTTATCCCTGACCGGAGATGCAAGTTCGTGTGTGTGT 1146

```

RESULT 15

US-09-170-331-3
Sequence 3, Application US/09170331C

Patent No. 6028175
GENERAL INFORMATION:

APPLICANT: Bunzow, James R.
APPLICANT: Grandy, David K.

TITLE OF INVENTION: A No. 6028175el Mammalian Methadone-Specific Opioid Receptor
TITLE OF INVENTION: Gene and Uses

FILE REFERENCE: 93-311-C
CURRENT APPLICATION NUMBER: US/09/170,331C

NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent Ver. 2.0

SEQ ID NO 3
LENGTH: 1452

TYPE: DNA

ORGANISM: Rattus norvegicus

FEATURE:

NAME/KEY: CDS
LOCATION: (182..(1282)

US-09-170-331-3

Query Match 22.5%; Score 361.8; DB 5; Length 1452;

Best Local Similarity 60.6%; Pred. No. 2e-87; Matches 616; Conservative 0; Mismatches 392; Indels 9; Gaps 1;

```

343 CCACCTTAGTGGCAACCTCTCCGACCATGCGGTCCGAACCCGACCGACTGGCGGAG 402
229 ccacttcaaggaaacttccctcctaagacgtaaccacccacacttccctca 288
403 AGACAGCCTGTGGCCCTCCAGACCGAGTCCCTCATGATCACAGGCATCAGCATATGC 462
289 tgcag-----tcaagcgcttctgccccttgtaactcaaggtacatcactgtag 339
463 CCTTACTCATGATGTGTGCGTGTGGGCTCTTCGAACTTCTGTGATGATGAT 522
340 gctcactcttgctgtgatcggggggtccttggaactcctcgtcatgtatgcat 399
523 TGTGATATCACCAAGATTAAGACTGACCAACATCTACATTTTCAACCTTGTGCG 582
400 cctcaggaaccagaatgaagacagctacccaactllacataatlaacttgcactg 459
583 AGATGCTTAGGACACAGTATCCCTGCTTCAGAGTGAATTAAGTGAAGGAAGAT 642
460 tgaatccttgctgtctaactgctcctcagggacacagacatcactgagcttcg 519
643 GCCATTGGAACATCTTTCGAAGATAGTATCTTCATATGATTAATATGATTTAC 702

```

Db 520 gccattgggaaagcaactctgcgaagactgcatatgactatgactactacaacatglttac 579
QY 703 CAGCAATTTACCCCTTGACACCATGAGTTGATGATACATGACAGTGTGCCACCTGT 762
Db 580 cagcaatttactctgacgcgcacagcgttagaccgtatggtctatctgcacccctat 639
QY 763 CAAGGCTTAGATTTCGGTACTCCCCGAATGCCAAATATATCAATGTCTGCACACTGAT 822
Db 640 ccgtgcccttgatgltgcgaacatcccaagccagcgtgtaattggtccatattggtc 699
QY 823 CCTCTCTTCAGCCATTGGTCTTCTGTAATGTTGATGCTACACAAATATACAGCAAG 882
Db 700 ccgtgcttcagtggtgtgtctctgttcgcataatggttcagcacaagtggaaagatga 759
QY 883 TTCCATAGATTGTACACTAAACATTCTCTCATCCAACTGTACTGGGAAAACCTGTGAA 942
Db 760 agagatcgaatgcgtgtgtagatccctgcacagactattgggacctgtattcgc 819
QY 943 GATCTGTGTTTCATCTTCGCTTCATATGCCAGTGTCTCATATACCGTGTCTATGG 1002
Db 820 catctgcatcttcccttcttccatcaaccctgtgtcatctctctgtctgtctacag 879
QY 1003 ACTGATGATCTTCGCTCAAGAGTGTCCGATGCTCTGTGCTCCAAAGAAAAGACAG 1062
Db 880 cctcatgattcgaagactcgtgtgtgtcgtctgtctcaggtcccggaagaagacgt 939
QY 1063 GAATCTTGAAGATCACACAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1122
Db 940 aaacctgcgcgtatcacctgcactgactgctgtgtgtgtgtgtgtgtgtgtgtgtgt 999
QY 1123 GACTCCCATTCACATTAGTCATCATTAAGCCTGTGTACAAATCCGAAACTAGCTT 1182
Db 1000 gacgcctgtgcagggt 1059
QY 1183 CCAGACTGTGTTTGCACTTGTGCTGCTAGTTACAAACAGCTGCTCAACCC 1242
Db 1060 tgcagttgcacatctcgt 1119
QY 1243 AGTCCTTTATGATTTCTGTGATGAAAACCTCAACGATGCTTCAGAGAGTTCTGTATCC 1302
Db 1120 catctctatgcttctgt 1179
QY 1303 AACCTCTTCAACATTTGACACAAACCTCCACTGCAATTCGTACAGACACTAGAGA 1359
Db 1180 ttcatccctgcaccggagagatgcaggttctgtatcgtgtgtgtgtgtgtgtgtgtgt 1236

Search completed: November 14, 2000, 22:43:21
Job time: 8623 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2000, 20:19:33 ; Search time 1825.6 Seconds
(without alignments)
3851.777 Million cell updates/sec

Title: US-08-305-518-7

Perfect score: 1610
Sequence: 1 CGGATGAGCGCTGTGAACT.....GCTCTGCACATTAGAGCCCG 1610

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_bal:*

2: gb_bal:*

3: gb_bal:*

4: gb_bal:*

5: gb_bal:*

6: gb_bal:*

7: gb_bal:*

8: gb_bal:*

9: gb_bal:*

10: gb_bal:*

11: gb_bal:*

12: gb_bal:*

13: gb_bal:*

14: gb_bal:*

15: gb_bal:*

16: gb_bal:*

17: gb_bal:*

18: gb_bal:*

19: gb_bal:*

20: gb_bal:*

21: gb_bal:*

22: gb_bal:*

23: gb_bal:*

24: gb_bal:*

25: gb_bal:*

44: em_htg7:*

45: em_htg8:*

46: em_htg9:*

47: em_htg10:*

48: em_htg11:*

49: em_htg12:*

50: em_htg13:*

51: em_htg14:*

52: em_htg15:*

53: em_htg16:*

54: em_htg17:*

55: em_htg18:*

56: em_htg19:*

57: em_htg20:*

58: em_htg21:*

59: em_htg22:*

60: em_htg23:*

61: em_hum3:*

62: em_hum4:*

63: em_hum5:*

64: em_hum6:*

65: gb_bal:*

66: gb_bal:*

67: gb_bal:*

68: gb_bal:*

69: gb_bal:*

70: gb_bal:*

71: gb_bal:*

72: gb_bal:*

73: gb_bal:*

74: gb_bal:*

75: gb_bal:*

76: gb_bal:*

77: gb_bal:*

78: gb_bal:*

79: gb_bal:*

80: gb_bal:*

81: gb_bal:*

82: gb_bal:*

83: gb_bal:*

84: gb_bal:*

85: gb_bal:*

86: gb_bal:*

87: gb_bal:*

88: gb_bal:*

89: gb_bal:*

90: gb_bal:*

91: gb_bal:*

92: gb_bal:*

93: gb_bal:*

94: gb_bal:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1610	100.0	1610	67	HUMOP10IDA
2	1562.6	97.1	2162	5	A87781
3	1553	96.5	2162	67	HUMWORI
4	1346.2	83.5	1473	66	HSU12569
5	1258	78.1	1881	3	PIGMOOPR
6	1167.8	72.5	1203	11	AF286024
7	1139.6	70.3	1415	3	BTU89677
8	1122	69.7	2228	5	A68824
9	1122	69.7	2229	12	MMU19380
10	1120.8	69.5	1586	12	RATMORA
11	1110.4	69.0	1610	12	MMU26915
12	1103	68.5	2397	12	RATRORE


```

|||||
Db 1021 CCAAGAAAGACAGGATCTTCAGAGATCACAGAGATGGTGGTGGTGGGCG 1080
|||
Qy 1107 TGTATATGCTGCTGGAGCTCCCATTCACATTTAGCTATCATTTAAAGCTTGTTACA 1166
|||
Db 1081 TGTATATGCTGCTGGAGCTCCCATTCACATTTAGCTATCATTTAAAGCTTGTTACA 1140
|||
Qy 1167 TCCGAAAGACTAGTTCAGAGCTGTTCTTGGACATTCGATGGTGTAGTTACACA 1226
|||
Db 1141 TCCGAAAGACTAGTTCAGAGCTGTTCTTGGACATTCGATGGTGTAGTTACACA 1200
|||
Qy 1227 ACAGCTGCTCAACCCAGCTCTTATGATTTCTGGATGAAAACCTCAACGATGCTCA 1286
|||
Db 1201 ACAGCTGCTCAACCCAGCTCTTATGATTTCTGGATGAAAACCTCAACGATGCTCA 1260
|||
Qy 1287 GAGAGTCTGTTTCCCAACCTCTTCCACATTTAGAGACAAACCTCAATTCGTC 1346
|||
Db 1261 GAGAGTCTGTTTCCCAACCTCTTCCACATTTAGAGACAAACCTCAATTCGTC 1320
|||
Qy 1347 AGAAGCTAGAGACCCCTCCAGGCGCAATAGATGAACTATCATTCAGCTAG 1406
|||
Db 1321 AGAAGCTAGAGACCCCTCCAGGCGCAATAGATGAACTATCATTCAGCTAG 1380
|||
Qy 1407 AAAATCTGGAAGCAGAAACTGCTCCGTTGCCCTAACAGGGTCTCATTCGACCTT 1466
|||
Db 1381 AAAATCTGGAAGCAGAAACTGCTCCGTTGCCCTAACAGGGTCTCATTCGACCTT 1440
|||
Qy 1467 CACCAAGCTAGAAACCCACATGATGTGAGAGCAGGTGCTTCAAGATGTGTAGAG 1526
|||
Db 1441 CACCAAGCTAGAAACCCACATGATGTGAGAGCAGGTGCTTCAAGATGTGTAGAG 1500
|||
Qy 1527 CTCTAATCTCTAGAAAGTGCCTCTTATGATTCACCACTCTTCTCTGAGCA 1586
|||
Db 1501 CTCTAATCTCTAGAAAGTGCCTCTTATGATTCACCACTCTTCTCTGAGCA 1560
|||
Qy 1587 CTCTGCTCTGACATTTAGAG 1607
|||
Db 1561 CTCTGCTCTGACATTTAGAG 1581
|||

RESULT 3
HUMORIX 2162 bp mRNA PRI 08-AUG-1994
LOCUS HUMORIX 2162 bp mRNA PRI 08-AUG-1994
DEFINITION Human mu opiate receptor (MOR1) mRNA, complete cds.
ACCESSION L25119
VERSION L25119.1 GI:452072
KEYWORDS Mu opiate receptor.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2162)
AUTHORS Wang,J.B., Johnson,P.S., Persico,A.M., Hawkins,A.L., Griffin,C.A.
and Uhl,G.R.
TITLE Human mu opiate receptor. cDNA and genomic clones, pharmacologic
characterization and chromosomal assignment
JOURNAL FEBS Lett. 338 (2), 217-222 (1994)
MEDLINE 94139928
FEATURES
SOURCE
Location/Qualifiers
1..2162
/organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_stage="adult"
/tissue_lib="lambda ZAP; Stratagene"
213..1415
/gene="MOR1"
213..1415
/gene="MOR1"
1..2162
/codon_start=1
/product="Mu opiate receptor"
/protein_id="AA20580.1"
/db_xref="GI:452073"
/translation="MDSAPPTNANCTDALAYSSCPAPSGWVNLSHLDNLSDP

```

1/31/94

```

CGPRTNLAGRDSICPTGSPSMITATITANALISVGVLEFNGFLMYIVRYTKMK
TATIVYENIALDALATSTLPPOSVAVYLAGTMEFTLTKIVISIDYMMFYSIFL
CTMSVDYRIAVLCHVRKALDRPNAITVNCMISSAIGIPMEATKRYQSGTD
CTLTFSPHTWENLVKICVFIFAFINPULITTYVCYLMILRLKSYMLEGSKENR
LRRTIRAVLVVAALVFIWPIHLYIVILKALVITPEFTQVSHFCIALGYNCSLA
PVLYAFIDENEFKRFREFCIPITSSNIQONSTRIRONTBHPSTANTVDRTHQLEHL
EAETAPLP"
BASE COUNT 563 a 566 c 455 g 576 t 2 others
ORIGIN
Query Match 96.5%; Score 1553; DB 67; Length 2162;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1567; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
Qy 36 GCGTATACGAGAGAGAAATGTACATGCTACGTCGGTCCCTCCGCTACAGCTCTC 95
|||
Db 9 GCGTATACGAGAGAGAAATGTACATGCTACGTCGGTCCCTCCGCTACAGCTCTC 68
|||
Qy 96 TCTGCTCAGCAGGACTGGTTTCTGTAAGAAACGAGAGAGCTGTGGCAGCGGGAAG 155
|||
Db 69 TCTGCTCAGCAGGACTGGTTTCTGTAAGAAACGAGAGAGCTGTGGCAGCGGGAAG 128
|||
Qy 156 GAAGCGCTGAGCGCTTGGAAACCGAAAGTCTCGGTCTCTGCTGCTACCTCGACAGC 215
|||
Db 129 GAAGCGCTGAGCGCTTGGAAACCGAAAGTCTCGGTCTCTGCTGCTACCTCGACAGC 188
|||
Qy 216 -GTGCGCGCGCGCGCGCTAGTACCATGACAGCAGCGTGGCGCCCGACGAGCCAGCAT 274
|||
Db 189 GGTGCGCGCGCGCGCGCTAGTACCATGACAGCAGCGTGGCGCCCGACGAGCCAGCAT 248
|||
Qy 275 TGCAGTATGCTGGCGCTTACTCAAGTGTCTCCAGACAGCCAGCGCGGTTCGTGGGTC 334
|||
Db 249 TGCAGTATGCTGGCGCTTACTCAAGTGTCTCCAGACAGCCAGCGCGGTTCGTGGGTC 308
|||
Qy 335 AACCTGTCCACTTAGATGAGCACTGTCCGACCCATGCGGTCCGAAACCGACCGACCTG 394
|||
Db 309 AACCTGTCCACTTAGATGAGCACTGTCCGACCCATGCGGTCCGAAACCGACCGACCTG 368
|||
Qy 395 GCGGGAAGAGACAGCGCTGCGCTCCGACCGGAGTCCCTCCATGATACCGGCATCAG 454
|||
Db 369 GCGGGAAGAGACAGCGCTGCGCTCCGACCGGAGTCCCTCCATGATACCGGCATCAG 428
|||
Qy 455 ATCATGCGCCCTACTCCATGCTGTGCGTGGGCTCTTCGGAACCTTCCTGGTCATG 514
|||
Db 429 ATCATGCGCCCTACTCCATGCTGTGCGTGGGCTCTTCGGAACCTTCCTGGTCATG 488
|||
Qy 515 TATGTATGTGACATACACCAAGATGAGACTGCGACCAACATCTACATTTCAACCTT 574
|||
Db 489 TATGTATGTGACATACACCAAGATGAGACTGCGACCAACATCTACATTTCAACCTT 548
|||
Qy 575 GCTGCGAGATGCGCTTGGACACAGTACCTGCGCTCCGAGAGTGAATTTACTATATG 634
|||
Db 549 GCTGCGAGATGCGCTTGGACACAGTACCTGCGCTCCGAGAGTGAATTTACTATATG 608
|||
Qy 635 GGAACATGCGCATTTGGAACCATCTTTCGAAGATAGATCTCCATGATTTACTATAC 694
|||
Db 609 GGAACATGCGCATTTGGAACCATCTTTCGAAGATAGATCTCCATGATTTACTATAC 668
|||
Qy 695 ATGTTACACCAATATTCACCTCTGACCATGAGTGTGATGATGATATTGCAAGTCTGC 754
|||
Db 669 ATGTTACACCAATATTCACCTCTGACCATGAGTGTGATGATGATATTGCAAGTCTGC 728
|||
Qy 755 CACCGTCAAGGCGCTTGTGATTCGCTGACCCGGAATGCAAAATATCAAGTCTGC 814
|||
Db 729 CACCGTCAAGGCGCTTGTGATTCGCTGACCCGGAATGCAAAATATCAAGTCTGC 788
|||
Qy 815 AACTGATCTCTCTACGACCATGTCTCTCTTAATGTATGATGCTACAAACAAATAC 874
|||
Db 789 AACTGATCTCTCTACGACCATGTCTCTCTTAATGTATGATGCTACAAACAAATAC 848
|||
Qy 875 AGCGAGTTCATGATGATTTGACACTAACTTCTCTATCCACCTGTGAGGAAAAC 934
|||

```



```

Db 61 AGCAGAGACTGTTCTGTAGTAAGAAACAGACAGACTGTGGAGGGGGAAGAGAGGCC 120
QY 164 TGAGAGCCTTGAACCCGAAAAGTCTGGTCTCTCTGGCTACCTGCGACAGC -GTGCCG 222
Db 121 TGAGAGCCTTGAACCCGAAAAGTCTGGTCTCTCTGGCTACCTGCGACAGCAGCGGTCG 180
QY 223 CCGGCGGTGTAGTACATGAGCAGAGGCTGCCCCACGAGCGCAGCAATTTGACTGA 282
Db 181 CCGGCGGTGTAGTACATGAGCAGAGGCTGCCCCACGAGCGCAGCAATTTGACTGA 240
QY 283 TGCCTTGGCTACTCAAGATTGCTCCCGACGACAGCCCGCGGTCTCTGGCTCAACTTGTG 342
Db 241 TGCCTTGGCTACTCAAGATTGCTCCCGACGACAGCCCGCGGTCTCTGGCTCAACTTGTG 300
QY 343 CCACCTTGAATGAGCACTGTCTCCGACCATGCGGTCCGACCGCAGCATCTGGCGGGAG 402
Db 301 CCACCTTGAATGAGCACTGTCTCCGACCATGCGGTCCGACCGCAGCATCTGGCGGGAG 360
QY 403 AGACAGCCTGTGGCTCCGACCGGAGAGTCCCTCATGATGACGGGCAATCAGATCATGCG 462
Db 361 AGACAGCCTGTGGCTCCGACCGGAGAGTCCCTCATGATGACGGGCAATCAGATCATGCG 420
QY 463 CCTCTACTCATCGTGTGCGGTGTGGGGCTCTTCGAAACTTCTGGTCAATGATGTAT 522
Db 421 CCTCTACTCATCGTGTGCGGTGTGGGGCTCTTCGAAACTTCTGGTCAATGATGTAT 480
QY 523 TGTAGATACACCAAGATGAGAGTGCACCAACATCTACATTTTCAACTTGTCTGGC 582
Db 481 TGTAGATACACCAAGATGAGAGTGCACCAACATCTACATTTTCAACTTGTCTGGC 540
QY 583 AGATGCTTGAACCACTCTTTCGAAAGATGATGATTCATAGATTACTATAATGATGTCAC 642
Db 541 AGATGCTTGAACCACTCTTTCGAAAGATGATGATTCATAGATTACTATAATGATGTCAC 600
QY 643 GCCATTTGGAACCACTCTTTCGAAAGATGATGATTCATAGATTACTATAATGATGTCAC 702
Db 601 GCCATTTGGAACCACTCTTTCGAAAGATGATGATTCATAGATTACTATAATGATGTCAC 660
QY 703 CAGATATTCACCTCTGACACCATGAGTGTGATGATGATGATGATGATGATGATGATGAT 762
Db 661 CAGATATTCACCTCTGACACCATGAGTGTGATGATGATGATGATGATGATGATGATGAT 720
QY 763 CAAAGCCTTGAATTCCTGCTACCTCCCGAATGCCAAATTTATCATGCTGCTCACTGAT 822
Db 721 CAAAGCCTTGAATTCCTGCTACCTCCCGAATGCCAAATTTATCATGCTGCTCACTGAT 780
QY 823 CCTCTCTCAGCACTTGTGCTCTCTGATGATGATGATGATGATGATGATGATGATGAT 882
Db 781 CCTCTCTCAGCACTTGTGCTCTCTGATGATGATGATGATGATGATGATGATGATGAT 840
QY 883 TTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 942
Db 841 TTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 943 GATCTGTGTTTCACTCTGCTGCTTCAATATGACAGTGTCTATCATACCTGCTGATG 1002
Db 901 GATCTGTGTTTCACTCTGCTGCTTCAATATGACAGTGTCTATCATACCTGCTGATG 960
QY 1003 ACTGATGATCTTGGCGCTCAAGAGTGTCCGATGCTCTGCTGCTCAAGAAAGAGAC 1062
Db 961 ACTGATGATCTTGGCGCTCAAGAGTGTCCGATGCTCTGCTGCTCAAGAAAGAGAC 1020
QY 1063 GAATCTTGAAGATGACCAAGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1122
Db 1021 GAATCTTGAAGATGACCAAGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1123 GACTCCATTCACATTTACGATCATATTAAGACCTTGGTTCAATCCAGAAATAGCTT 1182
Db 1081 GACTCCATTCACATTTACGATCATATTAAGACCTTGGTTCAATCCAGAAATAGCTT 1140
QY 1183 CCAGAGCTTCTTGGACATCTGCAATGCTCTAGAGTTACCAAAACAGCTCCCTCAACC 1242

```

```

Db 1141 CCAGACTGTTCTTGGCACTTCTGATGCTAGTGTACCAAAACAGTGCCTCAACC 1200
QY 1243 AGTCTTTATGATTTTGGATGATAAACTTCAACGATGCTTTCAGAGAGTTCTGTATCCC 1302
Db 1201 AGTCTTTATGATTTTGGATGATAAACTTCAACGATGCTTTCAGAGAGTTCTGTATCCC 1260
QY 1303 AACCTTTCACATTTGAGCAACAAACTCCACATCGAATTCGTGAGAACTAGAGACCA 1362
Db 1261 AACCTTTCACATTTGAGCAACAAACTCCACATCGAATTCGTGAGAACTAGAGACCA 1320
QY 1363 CCCTCCAGCGCCAAATACAGTGTAGTAACTAATCATCATGCTAGAAAATCT 1413
Db 1321 CCCTCCAGCGCCAAATACAGTGTAGTAACTAATCATCATGCTAGAAAATCT 1371

RESULT 5
LOCUS PIGMUOPR 1881 bp mRNA MAM 03-MAR-1999
DEFINITION Sus scrofa mu opioid receptor mRNA, complete cds.
ACCESSION L38645
VERSION L38645.1 GI:2072391
KEYWORDS SOURCE
ORGANISM
Sus scrofa
Pig.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 1881)
AUTHORS Rumpusich,M.S., Osinski,M.A., Brown,D.R. and Muraugh,M.P.
TITLE The porcine mu opioid receptor: molecular cloning and mRNA
distribution in lymphoid tissues
J. Neuroimmunol. 90 (2), 192-198 (1998)
99032385
MEDLINE 2 (bases 1 to 1881)
REFERENCE Osinski,M.A.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (19-SEP-1996) Mark A. Osinski, Veterinary Pathobiology,
University of Minnesota, St. Paul, MN 55108, USA
COMMENT On May 6, 1997 this sequence version replaced gi:1553056.
FEATURES
source
1..1881
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone="1d7"
/tissue.type="cerebral cortex"
/feature="PCR amplified"
237..1442
/codon_start=1
/product="mu opioid receptor"
/protein_id="AAB53770.1"
/db_xref="GI:1553057"
/translation="MDSADPRVANSCTDPFSPSSMCPVSPSPSWNFSLHGNLSD
PCIRNTELEGSDSLCPGSPSMVATILMALSIVCVGLGNLWVIVIRYK
KIRNITITNMLADALATSTLPGSVNLTGMPGTILCKIVISIDYNNETSTFT
LCITMSVDRIYACHPVKALDFRPNRAKILINCMNLLSSAIGLPVFMAITRYRNSI
DCALFTSHPTWYEWNLKICVFIFAFIMVLITIVYGLMIILKSVNLSGSKEDR
NMRIRIRVAVVAVIVICMTPIHIVILKALITIDETTFQVSMFCTALGYSNCL
NPVLAFLDENEFRCRFRFCIPSSYIEQONSRIORNRDHRSTANTVDRTNHOLEN
LEAFETALP."
BASE COUNT 463 a 533 c 423 g 462 t
ORIGIN
Query Match 78.1%; Score 1258; DB 3; Length 1881;
Best Local Similarity 88.4%; Pred. No. 0;
Matches 1425; Conservative 0; Mismatches 175; Indels 12; Gaps 5;
QY 4 ATGAGCCTCTCTGTAAGTGAAGTGGAGGGGCTTATACGAGAGAGATGTACATG 63
Db 1 ATGAGCTGTGTGATCTTAAGATGGAGGGGCAACAGAGAAATATGTCAAGAG 60
QY 64 CTCAGCTGGTCCCTCGCTGACGCTCTCTCTGTCTAGCCAGAGACTGGTTCTGTA 123
Db 61 CTTAGCTCT--CCTTCTGCTGACGCTCTCTGCTGCTGCTGCTGCTGCTGCTGTA 117

```

QY	124	AGAAACAGCAGACACTGTGGCAGCGCGAAAGACAGACCGGCTTGAGCGCTTGGAAACCCGAA	183
Db	118	AGAAAGTACAGAGACCCGTGGCGGGGGCTGAGAGAACGGGCTGAGGGCGCTGGAAACCCGAA	177
QY	184	AAGTCTGGTCTCTCTGGTACCTCGCAGCAGCGTGGCC---GCCGGGCGGTCACTAGCA	239
Db	178	AAGCCGGGTGATGGCGGTTACCTCACTGGGTGTGCCAGCCGCCACGGCGTCAACACCA	237
QY	240	TGACAGCAGCGCTGCCCCACGAGCCGACGCAATTGCACTGATGCTT--GGCTACT	296
Db	238	TGGACAGCAGCGCTGACCCCCGAAACGCCAGCAATTGCACTGATCCCTCTCGCCCTCTT	297
QY	297	CAAGTGTGTCCTCCAGACCCAGCCCGGGTTCCTGGGGTCAACTGTGCCACTTAAGATGGCA	356
Db	298	CAATGTGTCCTCCAGTACCTTAGCCCCAGCTCTCGGGTCAACTTCTCCACTTAAGAGGCA	357
QY	357	ACCTGTCCGACCCATGCGCGTCCGACCGCACCACTGGGGGAGAGACAGCCTGTGCTCC	416
Db	358	ACCTGTCCGACCCATGCAATTGCGAACCGACGAGCTGGGGGAGAGACAGCCTGTGCTCC	417
QY	417	CTCCGACCCGCACTGCTCCATGATCAAGGCCATCAAGATCATGGCCCTCTACTCCATCG	476
Db	418	CTCCGACCCGCACTGCTCCATGATCAAGGCCATCAAGATCATGGCCCTCTACTCCATCG	477
QY	477	TGTGGTGGTGGGCGCTCTTGAGAAACTCTCGTCACTGATGATGATGTGCAATACACA	536
Db	478	TGTGGTGGTGGGCTCTTGTGGAAACTCTCGTCACTGATGATGATGTGCAATACACA	537
QY	537	AGATGACACTGCGCACCAACATCTACATTTTCAACCTGCTGCGAGATGGCTTAGGCA	596
Db	538	AAATGAAACACTGCCACCAACATCATATTTTCAACCTGCTGCGGAGATGGCTTAGGCA	597
QY	597	CCAGTACCCCTCCCTTCAGAGTGTGAATTAAGTAAGGAAACATAGGGCAATTGGAAACA	656
Db	598	CCAGTACCCCTCCCTTCAGAGTGTCAATTAATGGAAAGTGGCCGTTTGGAAACA	657
QY	657	TCCTTTGGCAAGATAGTATCTCCATAGATTACTATTAACATGTTCCACAGCATATTCCACC	716
Db	658	TCCTGTGGCAAGATAGTATCTCCATAGATTACTATTAACATGTTCCACAGCATATTCCACC	717
QY	717	TCTGCAACCATAGAGTGTGATGATACATTGCATCTGCGCACCCCTGTGCAAGCGCTTAGATT	776
Db	718	TCTGCAACCATAGAGGTGTGATGATGATACATTGCATCTGCGCACCCCTGTGCAAGCGCGTGGACT	777
QY	777	TCCGACTCCCGCGAAAGGCCAAATTTTCATGTCGCAAGTGGATCCCTTTAGGCA	836
Db	778	TCCGCACTCCCGCGAAGGCCAAATATCAAGCTGTGCAAGTGGATCCCTTTAGGCA	837
QY	837	TTTGGTCTCTGTAATGTTTCATGGCTACAAACAATAATACAGCCAAAGGTTCCATAGATTGTA	896
Db	838	TTTGGTCTCTGTAATGTTTCATGGCTACAAACAATAATACAGGAAATGTTTCATAGATTGTA	897
QY	897	CACATAACATTCTCATTACCAACCGGTGACTGGGAAACCGTGGAAATCTGTGTTTCA	956
Db	898	CACATAACATTCTCACCACCAACCTGGTACTGGGAAACCGTGGTAAATCTGTGTTTCA	957
QY	957	TCTTCGCTTCATTATGCGCAGTGTCTATCTACGCTGTGCTATGAGCAGTATGATCTTGC	1016
Db	958	TCTTTCGCTTCATTATGCGCAGTGTCTCTCATCTACAGTGTGTTATGGCGTATGATCTTAC	1017
QY	1017	GCCCTAAGAGTGTCCGATCTCTCTGCGTCCAAAAGGAAAGGACAGAAATCTTCCAGAGA	1076
Db	1018	GCCCTAAGAGTGTTCGATCTCTCTGCGTCCAAAAGGAAAGGATTAAGAACTGTCCAGAGAA	1077
QY	1077	TCACAGAGATGTGCTGGTGGTGGCTGTGTTCACTGCTGTGCGAGACTTCCATTACAA	1136
Db	1078	TCACAGAGATGTGCTGGTGGTGGCTGTGTTCAATGTGCTGTGCGAGACTTCCATTACAA	1137
QY	1137	TTTACGTATCATTTAAAGCCTTGCTTACAAATCCGAGAAACTAGTCTCCAGACTGTTCTT	1196
Db	1138	TTTACGTATCATTTAAAGCCTTGCTTACAAATCCGAGAAACTAGTCTCCAGAGCTGTCTCT	1197

QY	1197	GGCACTTTCGATTTGCTCTAGATTACACAAMACAGTGGCTCAACCCAACTCCTTATGAT	1255
Db	1198	GGCACTTTCGATTTGCTCTAGATTATACCAACAGTGGCTCAACCCAACTCCTTATGAT	1257
QY	1257	TTCTGGATGAAAACCTTCAACAGATGCTTCAGAGAGTTGTATCCCAACCTCTTCACACA	1316
Db	1258	TTCTGGATGAAAACCTTCAACAGATGCTTCAGAGAGTTGTATCCCAACCTCTTCACACA	1317
QY	1317	TTGAGCAACAAAACCTCCACACTGCAATTTGCTCAGAACACTAGAGACCACCTCCACAGGCCA	1376
Db	1318	TTGAGCAACAAAACCTCCGCTCGAATTCCTCAAAAACACAGAGACCACCTCCACAGGCCA	1377
QY	1377	ATACAGTGGATAGAACTATATCATCAGCTAGAAAATCTGGAAGCAGAAACCTGCTCGTTGC	1436
Db	1378	ATACAGTGGATAGAACTATATCATCAGCTAGAAAATCTGGAAGCAGAAACCTGCTCGTTGC	1437
QY	1437	CCTAACAGGTTCTATGCGCATTCGACCTTCAACCAAGTTAGA-AGCCACCATGATGTG	1495
Db	1438	CCTAACCAAGTTCATGCGCATTCGACATTCCTCAATGAGCTTAAGACAGCCACCATCTACGTG	1497
QY	1496	GAAGCAGGTTCCTCAAGATGTGTAGAGAGCTTAATTTCTAGAAAAGTGCCTGCTTT	1555
Db	1498	GAAGCAGGTTCCTCAAGATGTGTAGAGAGCTTAATTTCTAGAAAAGTGCCTGCTTT	1557
QY	1556	TAGGTATTCACCAACTCTTTCTCTCTGTGGCCACTGTGCTCTGTGCACATTGAGAG	1607
Db	1558	GA-TGTATCAATATGTTTCTCTGTGGCCGCTGTGCTCTCACATGTGAGAG	1608

RESULT	6
AF286024	
LOCUS	AF286024 1203 bp mRNA PRI 03-AUG-2000
DEFINITION	Macaca mulatta mu opioid receptor mRNA, complete cds.
ACCESSION	AF286024
VERSION	AF286024.1 GI:9664878
KEYWORDS	.
SOURCE	rhesus monkey.
ORGANISM	Macaca mulatta Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopithecinae; Macaca. 1 (bases 1 to 1203) Miller,G.M. and Madras,B.K. Cloning of the Macaca mulatta mu opioid receptor Unpublished 2 (bases 1 to 1203) Miller,G.M. and Madras,B.K. Direct Submission Submitted (11-JUL-2000) Neurochemistry, New England Regional Primate Research Center, Harvard Medical School, One Pine Hill Drive, Southborough, MA 01772, USA
JOURNAL	location/Qualifiers
REFERENCE	1..1203
AUTHORS	/organism="Macaca mulatta"
TITLE	/db_xref="taxon:9544"
JOURNAL	/tissue_type="striatum"
	1..1203
	/codon_start=1
	/product="mu opioid receptor"
	/protein_id="AA97249.1"
	/db_xref="GI:9664878"
	/translation="MDSSAVPTNVSNCIDLAHSSCPARSPGSWNLSHLDGNLSDP CGPRDIDGDRSLCPPTGSPSMITATIALALSYICVGLFGNFIVMYIVRYTKK TATYIIFNLADALVTLPDSOYVLMGTWPFGLIKICYSIDYNNMTSIFPL CTMSVDRIAYCHPVKALDERTPRNAKIIVNCMAISLGDPVMEATYRKQSGID CTLFSHSRWNTMLKTCVEFAFIIMVILTYVGIMLLRLKRSVMASGSEKDN LRRTIRVLYVAVFICTPIYCIYVIYIKALKNTIPETPTYSMHRCIAGYNSCLN PEVLAPDENKRCFFRECIPTSSNIQDSNRIRONTKHPSANTVDTXNQLENL EAELAAPNP"
BASE COUNT	299 a 350 c 242 g 312 t
ORIGIN	

RITMVLVVAIVICWPIHIVYIKALITIPETPOTVSMHFCIALGYNSCLNPV
LYARLDEKFRKRFREFCIPSTIEQNSARIKRNTRHPSTANTVDRTNOLNLEEA
ETAPLP*
BASE COUNT 562 a 608 c 489 g 570 t
ORIGIN

Query Match 69.7% Score 1122: DB 12: Length 2229;
Best Local Similarity 83.4% Pred. No. 9.5e-282;
Matches 1324: Conservative 0: Mismatches 255; Indels 9; Gaps 4;

QY 4 ATGACCTCTGTGAACCTACTAAGTGGAGGGGGCTATACGACAGAGAGAAATGTAGATG 63
DB 20 AAGCCCTCCGCTGACTTCTAAGTGGAGGGGGATACAAAGAGAGAGAAATATGAGAG 79
QY 64 CTCAGCTGGTCCCTCCGCTGACGCTCTCTGTCTCAGCCAGAGAGTGTCTGTGA 123
DB 80 CTCAG-AGGTTCCATTCTGCTGCGGCTCTCTGTGTTCCACTAGGGCTTGTCTTGA 138
QY 124 AGAAGACAGAGAG-CTGTGCGAGGGGGGAAGAGGCGGAGAGGCGTTGGAACCGA 182
DB 139 AGAAGACAGAGAGCTAGGAGAGCTGTAGAGAGAGAGGCGGCGCTGGAACCGA 198
QY 183 AAGGTCTCG-GTGCTCTGTGCTACCTCGACAGCGTCCCGCGCGGCTCAGTACATG 241
DB 199 ACACCTTGAGTGTCTCTAGTACAGCCAGCGAGTCCGACAGAGCATTCAGAACATG 258
QY 242 GACAGCAGCGCTGCCCCCAGACGCGAGCAATTCGACTGATGCTTGGCGTACTCACT 301
DB 259 GACAGCAGCGCGCGCGGAGCAATTCGACTGCTGACCCCTTACCTCTCCCAAGT 318
QY 302 TGCTCCCGAGCAGCCAGCGCGGCTCTGCGGTCACTGTCCACTTATGAGCAACCTG 361
DB 319 TGCTCCCGAGCA-----CTGTGCTCTGTGCTCACTTGTCCAGGTTATGGAACAG 372
QY 352 TCCGACCCATGCGGTCCGAAACCGACAGCTGGGGGAGAGAGAGCGCTGCGCTCCG 421
DB 373 TCCGACCCATGCGGTCTCAACCGCAAGGGGCTTGGGGGAGAGAGCGCTGCGCTCCG 432
QY 422 ACCGCACTCCCTCATGATCAGGCGCATCAGATCATGCGCTTACTCCATCGTGTGC 481
DB 433 ACCGCACTCCCTCATGATCAGGCGCATCAGATCATGCGCTTACTCCATCGTGTGC 492
QY 482 GTGTGGGGGCTCTTGGAAACTTCTGTGATGATGATGATGATGATGATGATGATG 541
DB 493 GTGTGGGGGCTCTTGGAAACTTCTGTGATGATGATGATGATGATGATGATGATG 552
QY 542 AAGACTGCGACCAACATCTACATTTTCAACCTTGTCTGGAGATGCTTACCAACAGT 601
DB 553 AAGACTGCGACCAACATCTACATTTTCAACCTTGTCTGGAGATGCTTACCAACAGT 612
QY 602 ACCCTGCGCTTCCAGAGTGTGAATTAATGAGAAATGCGCATTTGGAACCATCTT 661
DB 613 ACGCGCGCTTCCAGAGTGTGAATTAATGAGAAATGCGCATTTGGAACCATCTT 672
QY 682 TGCAGATAGTATCTCCATAGATAGTATACATGTTACAGAGATATCAACCTGTGC 721
DB 693 TGCAGATAGTATCTCCATAGATAGTATACATGTTACAGAGATATCAACCTGTGC 732
QY 722 ACCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 781
DB 733 ACCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 792
QY 782 ACTCCCGCAAAATGCAAAATTTCAATGCTGCAACTGTGATCTCTTTCAGCCATGCT 841
DB 793 ACCCCCGCAAAATGCAAAATTTCAATGCTGCAACTGTGATCTCTTTCAGCCATGCT 852
QY 842 CTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 901
DB 853 CTGCGCGTAATTTTATGAGCAACCAAAATACAGGAGGGGCTCATGATTTGCAACCTTC 912
QY 902 ACATTTCTCATCAACCTGTGATGAGAAACCTGTGAAAGATCTGTGTTTCATCTTC 961

DB 913 ACTTCTCATCCACATGAGTACTGGGAGAACCTGCTCAAAATCTGTCTCATCTTC 972
QY 962 GCTTCATTTATCCAGTGTCTATCATTTACCGTGTCTATGAGACTATGATGTGGCCTC 1021
DB 973 GCTTCATTTATCCAGTGTCTATCATTTACCGTGTCTATGAGACTATGATGTGGCCTC 1032
QY 1022 AAGATGTCCGATCTCTGCTCCCAAGAAAGAGAGAGATCTTGAAAGATCAC 1081
DB 1033 AAGATGTCCGATCTCTGCTCCCAAGAAAGAGAGAGATCTTGAAAGATCAC 1092
QY 1082 AAGATGTCCGATCTCTGCTCCCAAGAAAGAGAGAGATCTTGAAAGATCAC 1141
DB 1093 AAGATGTCCGATCTCTGCTCCCAAGAAAGAGAGAGATCTTGAAAGATCAC 1152
QY 1142 GTTCATTTAAAGCTTGTGTTCAATTCGAGAACTACGTTCCAGAGTGTCTTGGCAG 1201
DB 1153 GTTCATTTAAAGCTTGTGTTCAATTCGAGAACTACGTTCCAGAGTGTCTTGGCAG 1212
QY 1202 TTTGCTATGCTGTAGTGTACCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1261
DB 1213 TTTGCTATGCTGTAGTGTACCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1272
QY 1262 GATGAAATCTCAAG 1321
DB 1273 GATGAAATCTCAAG 1332
QY 1322 CACAAAACTCCTGCTGAGTGTGAGAACTACGAGAGAGAGAGAGAGAGAGAGAG 1381
DB 1333 CACAAAACTCCTGCTGAGTGTGAGAACTACGAGAGAGAGAGAGAGAGAGAGAG 1392
QY 1382 GTGATAGAGATCAATCAGTGTAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1441
DB 1393 GTGATAGAGATCAATCAGTGTAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1452
QY 1442 CAGGCTCTATGCTCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1501
DB 1453 CAGGCTCTATGCTCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1512
QY 1502 GGTGCTCTCAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1561
DB 1513 GGTGCTCTCAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1572
QY 1562 ATCCAAACCTTCTCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1589
DB 1573 ATCCAAACCTTCTCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1600

RESULT 10
RATMORA
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
FEATURES
source
1. .1586
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/tissue_type="Whole brain"
210. .1406
/codon_start=1
/evidence=experimental

MEDLINE 95377399
REFERENCE 2 (bases 1 to 1610)
AUTHORS Pan, Y.-X.
TITLE Direct Submission
SUBMITTED (11-MAY-1995) Ying-Xian Pan, Neurology, Memorial
Sloan-Kettering Cancer Center, 1275 York Ave., New York, NY 10021
USA

BASE COUNT	373 a	476 c	368 g	393 t
ORIGIN				

[illegible]

QY	480	GGGTCGTCGGGCTCTTGGAAACCTTCGTGCATGATGTGATGTGCACATACACCAAGA	539	RESULT	12
	1			RATROB	
Db	518	GTGTAGTGGGCTCTTTGGAACTTCCTGTGCATGATGTGATGTGAAGATATACCAAAA	577	LOCUS	
				RATROB	2397 bp
				DEFINITION	Rat mRNA for rat oploid receptor B, complete cds.
QY	540	TGAACACTGCCACACACATCTACATTTTCAACCTTCCTGTGGCAGATGCTTACGCCACA	599	ACCESSION	D16349

Db	1074	ATTATGCTGCTGGAGAACCCCAATCCACATCTACGTCATCATCAAAAGCGCTGATCAGAT	1133
Qy	1168	CCAGAAATCACTAGCTTCAGACTGTTCTTGCGCACTTCTGCATTTGCTCTAGGTTACACAA	1227
Db	1134	TCCGAAACACCATTTCTCAGACCGGTTTCTTGCCACTCTGCATTTGGCTTTGGGTTACACAA	1193
Qy	1228	CAGTGGCTCAACCCACTCCTTTATGATTTCTGATTTGATGAAACTTCAAACGATGGCTTAG	1287
Db	1194	CAGTGGCTGATCATCACTTTCTTTTACGCTTCTCGATGAAACTTCACAGCGATGCTTAG	1253
Qy	1288	AGATTTCTGATCCCAACCTCTTCCAACTTGGAGACAACAACTCCACTCGAATCTGCA	1347
Db	1254	AGAATTCTGCATCCCAACCTCTGTCAGATCGAACAGCAAACTCCACTCGAGTCCGCA	1313
Qy	1348	GAACTAGACACCAACCCCTCAAGGCGCAATACAGTGGATAGAACTAATCATCACTAGA	1407
Db	1314	GAACTAGAGGAAATCATCCCTCCACAGGCTAATACAGTGATCGAACTAACCAACCACTAGA	1373
Qy	1408	AAATCTGGAGACGAAATCTGCTCGTTGCCCTTAACAGGCTCTCATGCACTTCCGACCTTC	1467
Db	1374	AAATCTGGAGGACGAAATCTGCTCATTTGCCCTTAACGGGCTCTCACACCATCCGACCTTC	1433
Qy	1468	ACCAAGCTTAGA 1480	
Db	1434	GCTAAGCTTGATA 1446	

RESULT 14					
LOCUS	RATMOPROID	1401 bp	mRNA	ROD	24-JAN-1994
DEFINITION	Rat mu opioid receptor mRNA, complete cds.				
ACCESSION	L22455				
VERSION	L22455.1	GI:437671			
KEYWORDS	mu opioid receptor.				
SOURCE	Rattus norvegicus (strain Sprague-Dawley)				
ORGANISM	Rattus norvegicus				
	Eumkaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi				
	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;				
	Rattus.				
REFERENCE	1 (bases 1 to 1401)				
AUTHORS	Thompson,R.C., Mansour,A., Aki,H. and Watson,S.J.				
TITLE	Cloning and pharmacological characterization of a rat mu opioid				
	receptor.				
JOURNAL	Neuron 11 (5), 903-913 (1993)				
MEDLINE	94059560				
FEATURES	Location/Qualifiers				
source	1..1401				

```

BASE COUNT      330 a      434 c      312 g      325 t
ORIGIN
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/sex="male"
/tissue_type="olfactory bulb"
/tissue_id="lambda ZapII from Stratagene"
170. .1366
/codon_start=1
/product="mu opioid receptor"
/protein_id="AA16075.1"
/db_xref="gi:437672"
/translation="MDSSTGPGNTSDGSDPLAQASCSAPBSMTLNSHYDGNQSDPGG
LNRIQLGGSDSLCPQIGSPSWVATITNALSYICVVGLEFENFLVMYIVITTKTR
TNIILFNILADALATSTLPQSVNVAITMGWPFQILKIVISIDYINMFSITFLCT
MSVRYIAYCKVKAIDRTPRNARKIVNWCMIISLADGLVPMATTKYSGSICDT
LTFSHPITWYENHLKICVEIFAFIPMPVILIVCGYGLMILKSVMLSGSKERINR
RITMRLLVVAVFIVCMTPIHIVIKILITIPETPQVSMHCIALGYNSCLNPV
LYALDENFKRCFREFCIPSTIEQGNSTRVQNTREHPSTANTVDRITNQDLENLR
ETAPLP"

```

Query Match	64.58;	Score 1039;	DB 12;	Length 1401;
Best Local Similarity	84.98;	Pred. No. 4e-260;		
Matches 1189;	Conservative	0;	Mismatches 205;	Indels 7;
				Gaps 2;

[illegible]


```
Db 1077 GTTTCGATCCCAACCTGCTCCACGATCGAAGCAAACTCCACTCGAGTCCGTACAGA 1136
OY 1351 CACTAGAGACCAACCCCTCCACGGCCAAATACAGTGAATAGAACTAAATCATCAGCTAGAAAA 1410
Db 1137 CACTAGGGAAACATCCCTCCACGGCTAATACAGTGAATCGAACTAAACACACAGCTAGAAAA 1196
OY 1411 TCTGAAGCAGAACTGCTCCGTGCCCCAAGGGTCTCATGCCATTCGACCTTCACC 1470
Db 1197 TCTGAGGCGAGAACTGCTCAATGCCCTAATGCGTCTCACACCACTCCAGACCTCGCT 1256
OY 1471 AAGCTTAGAAGCCACCATGATGTGGAAGCAGGTTGCTCAAGAAATGTTAGAGGCTCT 1530
Db 1257 AAGCTTAGAGGCGCCCATCTAGTGAATCAGGTTGCTCAGGGTGTGTGGAGGCTCT 1316
OY 1531 AATCTCTAGGAAGTGGCTGCTTTAGGTATCCAACTCTTCCCTCTGAGGCACTCT 1590
Db 1317 GGTTCCTGAGAAA--CCATCTGATCCCTGATCAAAAGTCATTCCTCTGTGCTACTTC 1373
OY 1591 GCTTGCACTTAGAG 1606
Db 1374 ACTTGCACTTAGAG 1389
```

Search completed: November 14, 2000, 22:42:27
Job time: 8574 sec

PT diagnosis, treatment and drug screening.

XX Claim 5; Page 208-210; 266pp; English.

XX A CDNA library constructed from human caudate nucleus mRNA was screened with rat mu opioid receptor cDNA under conditions of low stringency. One positive clone included the sequence given in CC 089226, encoding a mu opioid receptor MOR (R71964). The cDNA is used for prodn. of recombinant MOR, in gene therapy, etc.

XX Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T; 0 other:

Query Match 100.0%; Score 1610; DB 16; Length 1610;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGATGAGCTCTGTGACTACTAGTGGAGGGGCTATACGAGAGAGATGTCTAG 60
DB 1 cggatgagcctctgtgaactactaagtgaggagggctatacagagaggaatgtag 60
QY 61 ATGCTCACTGGTCCCTCCGCTGAGCTCTCTGTCTCAACCCAGAGACTGTTCT 120
DB 61 atgctcagctggtccctccgctgacgctctctctgtctcagcagagactggttct 120
QY 121 GTAGAAACAGAGAGGCTGTGGCAGCGGCGAAAGAGCGGCTGAGGGCTTGAACCC 180
DB 121 gtaagaacaacagagagctgtggcagcg99cgaagaagcggctgagggcttgaacc 180
QY 181 GAAAGTCTCGGTGCTCTGTGCTACCTGCGACAGCGTGGCCGCCGCGCTGATGACAT 240
DB 181 gaaagtctcggtgctctgtgtctgtctacgacagcgtgcccgcgctgagtaacct 240
QY 241 GGACAGCGCGCTGCGCCCGACGAGAGCGCAATGCTATGCTTGGCTTACTCAAG 300
DB 241 ggaacagcgcgctgccccgacgaacgacgaatgctatgcttggcttactcaag 300
QY 301 TTGCTCCCGACGACCGACCGCGGTTCTGGGTCACTTGTCCCACTTATGATGCGACCT 360
DB 301 ttgtctcccgacgacccgaccccggttctgtgtcaactgttcccacttatagagaaact 360
QY 361 GTCCGACCCATGCGGTCCGAAACCGACGACCTGGGCGGAGAGAGAGCGTGTGCCCTCC 420
DB 361 gtccgacccatgctgtccgaacccgacgacccgtggcgagagagacgcttgcctcc 420
QY 421 GACCGGAGTCCCTCCATGATCAGCGGCATCAGATGAGCGCTTACTCATGCTGTG 480
DB 421 gaccggagctccctccatgatacagccatcagatcagatgacccctcactcactcgtg 480
QY 481 CGTGTGGGCTCTTCGGAACCTTCTGTCATGTATGTATGATGTCAGATACCAAGAT 540
DB 481 cgtgtgggctcttcggaaccttctgtctgtatgtatgtatgtcagataccaagat 540
QY 541 GAAGACTGCCAACATCTACATTTTCAACCTTCTGCGAGATGCCCTTAGCCACGAG 600
DB 541 gaagactgccaaacatctacatttcaaccttctcggagatgaccttagccacag 600
QY 601 TACCTGGCCTTCCAGATGTGAATTACTTATGGAAACATGCGCATTTGGAACATCCT 660
DB 601 tacctggccttccagagtgatgaattacttaacatgttcacacgacatattacacctctg 660
QY 661 TTGCAAGATAGATCTCATATGATTACTATATACATGTTACACAGCATTTACCCCTCG 720
DB 661 ttgcaagatagatctcatatgattactataactatgttcacacgacatattacacctctg 720
QY 721 CACCATGAGTGTGATCATATGATGTCGACCCCTGTCAAGGCGCTTATGATTTCCG 780
DB 721 caccatgagtgtgtatgatacatgacgtctgcacacctgtcaaggccttagattccg 780
QY 781 TACTGCCCGAAATGCGAAATATATCAATGTCTGCAACTGATGCTCTTTCAGCCATTGG 840
DB 781 tactgcccgaaatgccaatataatcatatgctgcacactgattcctcttcagcattgg 840

QY 841 TCTTCTGTAATGTTCAATGCTACACAAATATACAGGAGGTTCCATAGATGTACACT 900
DB 841 tcttctgtaatgttcaatgctacacaaatatacaggaggttccatagatgtacact 900
QY 901 AACATTTCTCATCCACACCTGTAAGTGGGAAAACCTGCTGAGATCTGTGTTTATCTT 960
DB 901 aacattctcatccaaactgtactggaanaacctgtgagatctgttttcatctt 960
QY 961 CGCCTTCAATTATGGCAGTGCATCATATACCGTGTGCTATGAGATGAGATCTTCCGCT 1020
DB 961 cgccttcaattatggcagtgcatcatataccgtgtgctatgagatgagatcttccgct 1020
QY 1021 CAAGAGTCCGCAATGCTCTGTGGCTCCAAAGAAAGAGACGATCTTCAAGATATAC 1080
DB 1021 caagagtcccgcaatgctctgtggctccaaagaaagagacgaaatcttcgaagatcac 1080
QY 1081 CAGATGTGCTGT 1140
DB 1081 cagatgtgctgt 1140
QY 1141 CGTCACTTAAAGCCTGTGTTACAAATCCCAAGAAACTACGTTCCAGACTGTTTCTTGGCA 1200
DB 1141 cgtcactttaaagcctgtgttacaatcccaagaaactacgttccagactgtttcttggca 1200
QY 1201 CTTCTGCAATGCTCTAGGTTACACAAACAGCTGCTCAACCCAGTCTTATGATTTCT 1260
DB 1201 cttctgcaatgctctaggttacacaaacagctgctcaaccagctcttatagtcttct 1260
QY 1261 GGATGAAACTTCAACGATGCTTCAGAGAGTTCTGTATCCCAACCTTTCACATTGA 1320
DB 1261 ggaatgaaacttcaacgatgcttcagagagttctgtatcccaacctttcacattga 1320
QY 1321 GCAACAAACCTGCATGTAATTCGTGAGACATGAGACACCCCTCAGGCGCAATAC 1380
DB 1321 gcaacaaacctgcataatctgtgagacatgagacacccctcagcgccaatac 1380
QY 1381 AGTGATGAGATATATATCATGATGAGAAATCTGGAACAGAACTGCTCCGTTGCTA 1440
DB 1381 agtgatgagatataatcatgatacagtaagaatctggaagcagaactgtccgttcccta 1440
QY 1441 ACAGGCTTCATGCCATTCCGACCTTTCACCAAGCTTAAAGCCACCATGTATGTGAAGC 1500
DB 1441 acaggcttcattgccattccgaccttcccaagctttaaagccacatgtatgtgaagc 1500
QY 1501 AGGTGCTTCAAGATGTGTGAGAGCTCTAATTCCTAGGAAAGTGCCTGTTTAGT 1560
DB 1501 aggtgcttcaagatgtgtgagagctctaattcctaggaagagtgctgtttagt 1560
QY 1561 CATCCAACTCTTTCCTCTGCGCAGCTGTGCTGACATTTAGAGGCG 1610
DB 1561 catccaaactcttctctctctcgtgcacactctgtctgcacattagagcg 1610

RESULT 2
V61984
ID V61984 standard; cDNA; 2162 BP.
XX AC
XX V61984.
XX 11-JAN-1999 (first entry)
DE Human mu-opioid receptor cDNA.
XX
XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KW psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KW cocaine; inherited alcoholism; human; ss.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 213..2040
FT CDS
FT /*tag= a

FT		/product= "mu-opioid receptor"
FT	misc-feature	502..503
FT		/tag= b
FT	misc-feature	/note= "Site of intron 1"
FT		855..856
FT		/tag= c
FT	misc-feature	/note= "Site of intron 2"
FT		1376..1377
FT		/tag= d
FT		/note= "Site of intron 3"
XX		
PN	W09833937-A2.	
XX		
PD	06-AUG-1998.	
XX		
PF	02-FEB-1998;	98MO-DE00382.
XX		
PR	03-FEB-1997;	97DE-1003925.
XX		
(DELBA)	DELBUECK CENT MOLEKULARE MEDIZIN MAX.	
PI	Hoehe M, Wendel B;	
XX		
DR	WPT. 1998-437487/37.	
XX		
PT	New genomic and cDNA sequences encoding human mu-opioid receptor -	
PT	used, e.g. to predict pre-disposition to addiction and for	
PT	development of analgesics, anaesthetics and anti-addiction agents	
XX		
PS	Claim 8; Page 14-15; 26pp; German.	
CC		
XX	This sequence encodes a novel human mu-opioid receptor. This sequence and	
CC	its variants, polymorphisms and mutants are used in a method for	
CC	detecting predisposition to disease, particularly addictive disease, by	
CC	isolating DNA from a sample, genotyping selected positions and comparing	
CC	with a reference DNA. Such sequences are used to develop analgesic,	
CC	anaesthetic, anti-addictive and psychopharmaceutical agents, to construct	
CC	genes and vectors, particularly for pharmaceutical development, to	
CC	develop diagnostic kits for predicting risk of addiction, response to	
CC	analgesics or anaesthetics, or development of side effects from a drug.	
CC	Particular applications are to determine risk of addiction to opiates or	
CC	cocaine, or of developing inherited alcoholism.	
SQ		
Sequence	2162 BP; 562 A; 565 C; 458 G; 575 T; 2 other;	
.		
Query Match	97.1%; Score 1562.6; DB 19; Length 2162;	
Best Local Similarity	99.7%; Pred. No. 0;	
Matches 1576; Conservative	0; Mismatches 4; Indels 1; Gaps 1	
OY	28 TGGGAGGGGGCTATACGCAGAGAGAATGTCAAGATCCTCAGCTCGGTCGCCCTCGGCTGA	87
Db		
	1 tgggaggggggcgttaacgaagaagaaatgcaatgctcagctcggtcccttcgcgtga	60
OY	88 CGCTCCTCTCTGTCTCAGCGCAGGACACTGTTTCTGTAAAGAAACGACGAGCTTGCGCA	147
Db		
	61 cgctcctctctgtctcagcagcagactggttctgtaagaacaagcagagtgtgycagc	120
OY	148 GCGCAAAGAACCGGCTGAGCGGCTTGAAACCCGAAAAGTCTCGGTGCTCTGGCTA	207
Db		
	121 ggcgaagaagaaacggtctgagcgtcttgaaaccgaaaagtctcgtgctcgtctacct	180
OY	208 GCGCACAGC-GTCCGCCGCCGGCGCTGATACCATGACACGACGCTGCCGCCACGAAC	266
Db		
	181 cgcacaaggcggccccgccgcgctaagtaaccaatggaacagcagcgtcgtcccacaagac	240
OY	267 CCAGCAATTGCACTGATGCTTGCTTGACCTACTCAAGTTGCTCCCCAGACACCAGCCGGTT	326
Db		
	241 ccagcaaatgcaactgatgctcttgctgtaactcaaatgtctccccaagcaaccgccggtt	300
OY	327 CCTGGGTCACTTTGCTCCACTTAGATGGACAACCTGTTCGACCCCATGCGGTTCGAACCGCA	386
Db		
	301 cctgggtcaactgtctccacttatagatgcaacctgtccgaaccatgagttcgaacgcga	360

OY	387	CCGACCTGGGCGGAGAGACAGCCTTGGCCCTCCACCGGACAGTCCCTCATGATCAGG	446
Db	361	ccaaactcgggacggagagaaacagccctctgcccctcgaccgagctccctccatgatacgg	420
OY	447	CCATCAGCATCATGAGCCCTTACTCCATGCTGAGTGGGTGGGCTCTTCGAAATCTCC	506
Db	421	ccatcaagatcatgagcccttactccatctgctggtggtggtctcttgaaacttcc	480
OY	507	TGTCATGATGATGATTGTTCAGATACACCAAGATGAGACTGCCACCAACATCTACATT	566
Db	481	tgcatactgatagtatgtatgctaaatacacaagaataaagactgccacaacatctcaatt	540
OY	567	TCAACCTGGCTGCGGACGAGATGCTTAGCCACAGTACACCTGGCCCTCCAGAGTGAATT	626
Db	541	tcaaccttgcctcggagcaagctcttagccaagaataccctgccttccagaagtggaaat	600
OY	627	ACCTAATGGGAACATGGCCATTITGGAACCATCCTTTGCAAGTACTGATCTTCATAGAT	686
Db	601	acctaatgggaacatgagccatttggaacacatcctttgcaagtagtattccataagatt	660
OY	687	ACTATACATGTTTACCAGATATTTCACCCCTCGACCACTAGTGTGTATGATGATCATG	746
Db	661	actataacatgitttacaagaatataccaacctctgcaccaatgagttgatcgaatacttg	720
OY	747	CAGTCTGCCACCCGTCAAGGCTTAGATTTCGGTACTCCCGGAATGCCAAATATTATCA	806
Db	721	cagctgcgcacccctgttaagcctctgattcttcgtaattcccgaaatgccaataataca	780
OY	807	ATGTCGCAACTGGATCTCTCTCTTCAAGCCATGCTTCTCTGTAATGTTATGGCTACAA	866
Db	781	atgtctgcaactgtaattcctctcttcagccaattgctctcttatagtttcatacgaataa	840
OY	867	CAAAATACAGGCAAGTTCATAGATTGTAACATAACTTCCTATCCAACTGGTACT	926
Db	841	caaaatcacggcaaggttccataagatttgtaacatacaatcctcatccaacccggtact	900
OY	927	GGGAAACCTGCTGAAGATCTGTTTTCATCTTCGCCCTTCAATTAGCAGTGCATCA	986
Db	901	gggaaaacctcgtgaagatctgctttcatctcttcgaccttcatatgcagtgctcatca	960
OY	987	TTACCGTGTGCTATGACCTGATATATCTTCGGCTCAAGAGTTCGGCATGCTCTGGCT	1046
Db	961	ttaaccgtgtgtctaaagactgaatcttgccgtccaaagatgctccgaatgcctctgct	1020
OY	1047	CCAAGAAGAAAAGACAGAAATCTTGAAGAGTACACCGATGCTGCTGGTGGTGGCTG	1106
Db	1021	ccaaagaaaaggacaggaatctctcgaaagatacccaagatgctgctggtggtggtg	1080
OY	1107	TGTTCAATGCTGTGCTGGACTCCCATTCACATTTAGTCAATCAATTAAGCCTTGTTACAA	1166
Db	1081	tgttcaatgctgtctgtgaccccatccaatcaattacgtcatcaataaagccctggttcaaa	1140
OY	1167	TCCAGAAACACAGCTTCCACACTGTTTCTTGGACTTCCTGCAATGCTCTAGGTTACAAA	1226
Db	1141	tccagaaactaagttccagacagcttctcttgagcaattcgcattgctctaggttaacaaa	1200
OY	1227	ACAGCTGCTCAACCCACAGTCTTTATGCAATTTCTGGATGAAAACTTCAAGAGATCTTCA	1286
Db	1201	acagctgcctaaacccagctccttatagtcaattctgtatgaaacttcaaaacgaatgcttca	1260
OY	1287	GAGAGTCTGTATGCCAACCTCTTCCAACATTTGAGCAACAAATCCCACTGGAATTGCTC	1346
Db	1261	gagagctctgtatctcaaacctcttccaacatgagaaataaaactccactcgaattctctc	1320
OY	1347	AGAGACTTAGAGACCAACCCCTCCACGGCCCAATACAGTGGATGGAATCAATCATCAGCTAG	1406
Db	1321	agaagacttagagcaaacccctccacgccaataaagttgataagaaataatcatcaagctag	1380
OY	1407	AAATCTGGAGGAGAAATCTGCTCGTGGCTTACAGGSGTTCATGCCATTTCCGACTT	1466
Db	1381	aaatctggagagcaaaactgctctctgtccctcaaaaggttctcatgtcatcttcgaactt	1440


```

Db 781 atgctgcaactggaatccctctcctcagccattggtcttcctcctaatgtatcagtacaa 840
Qy 867 CAAATATAGCGAAGGTTCCATAGATTGTACACTAACCTTCTCATCTCAACCTGTACT 926
Db 841 caaatataaggcaaggtccatagattgtacactaacatctctcatcaaaccttgact 900
Qy 927 GGGAAACCTGCTGATGCTGTGTTTTCATCTTGCCCTTCAATATAGCAGTGCATCA 986
Db 901 gggaaaacctgtgaagatcgtgttttccatcttcgcctcatatagcagtgctacaa 960
Qy 987 TTACCGTGTGATGAGTATGATCTTGCCCTCAGAGTGTCCGATGCTCTGTGCT 1046
Db 961 ttaccgtgtgtatgactgtatgtatcttgccctcaagaagtgtccagctgtctctgt 1020
Qy 1047 CCAAGAAAGAGACAGAACTTTGGAAGATCACCAGATGCTGCTGTGTGTGCTG 1106
Db 1021 ccaagaagaagacagatcttcgaagaatcaccagaagtgtgtgtgtgtgtgtgt 1080
Qy 1107 TGTTCATGCTGCTGATGCTCCATTCATTCATTCATTCATTCATTCATTCATTCAT 1166
Db 1081 tttcatcgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1140
Qy 1167 TCCGAGAACTAGCTTCCAGACTGTTTCTTGCGACTTGTGCTAGTGTACACA 1226
Db 1141 tcccaagaactacgttccagactgttctctgtgcaactctgtcctagtctgtacaa 1200
Qy 1227 ACAGCTGCTTACCCCATCTTATGATCTTGTGATGGAAGAACTCAAGATCTTCA 1286
Db 1201 acagctgtctcaaccacgtctctatgtatctgtatgtatgtatgtatgtatgt 1260
Qy 1287 GAGAGTTCTGATCCCACTCTTCCACATTCAGCAACAAACCTCACTGATTCGTC 1346
Db 1261 gagggttctgtatcccaacctcttccaaatgtgcaacaaacctcctgaatgtct 1320
Qy 1347 AGAACACTAGAGACACCCCTCCACGCGCAATACAGTGAATAGAACTATCATCAGCTAG 1406
Db 1321 agaacactagagacacccctccacagccatacagtgatagaaactaatcatcagctag 1380
Qy 1407 AAAATCTGAGACGAACACTCTCCGTGCTCCCTTACACAGGCTCTCATTCGCTACT 1466
Db 1381 aaatctggaagcagaactcctcgtgtccctcaagagctctcctcctcctcctc 1440
Qy 1467 CACCAAGCTTGAAGCCACATGATGTGAAGAGCTTGCTCAAGATGTGTGAGAG 1526
Db 1441 caccagaacttagaagccacatgtatgtggaagcaggtgtgtcctcaaatgtgtgaag 1500
Qy 1527 CTCTAATCTCTAGAAAGTCTGCTTTTGTAGTCAACCTCTTCTCTGTGCGCA 1586
Db 1501 ctctaatctcttagaagagtgctactctttagtcatcctcaacctcttctcctgtgcca 1560
Qy 1587 CTCTGCTCTGCACATAGAGG 1607
Db 1561 ctctgctctgcacattagag 1581

```

RESULT 4
V61985
ID V61985 standard; cDNA; 2162 BP.

XX V61985;
XX
XX 11-JAN-1999 (first entry)
DE Human mu-opioid receptor cDNA variant 1.
XX
XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KM predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KM psychopharmacological agent; diagnostic; side effect; drug; opiate;
XX cocaine; inherited alcoholism; human; ss.
XX Homo sapiens.
OS Synthetic.
XX

```

FH Key Location/Qualifiers
FT CDS 213..2040
FT /tag= a
FT /product= "mu-opioid receptor"
FT misc_feature 502..503
FT /tag= b
FT /note= "Site of intron 1"
FT misc_feature 855..856
FT /tag= c
FT /note= "Site of intron 2"
FT misc_feature 1376..1377
FT /tag= d
FT /note= "Site of intron 3"
FT mutation 41
FT /tag= e
FT /note= "Wild type G is replaced by T"
PN MO9833937-A2.
PD 06-AUG-1998.
XX
PF 02-FEB-1998; 98WO-DE00382.
PR 03-FEB-1997; 97DE-1003925.
XX
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
PI Hoehe M, Wendel B:
PI
XX
DR WPI: 1998-437487/37.
XX
PT New genomic and cDNA sequences encoding human mu-opioid receptor -
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
XX
PS Claim 8; Page -: 26pp; German.
XX
CC This sequence encodes a novel human mu-opioid receptor in which a G
CC nucleotide at position 41 of the wild-type sequence represented in
CC V61984 is replaced by a T. The wild-type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
CC anti-addictive and psychopharmacological agents, to construct genes and
CC vectors, particularly for pharmaceutical development, to develop
CC diagnostic kits for predicting risk of addiction, response to analgesics
CC or anaesthetics, or development of side effects from a drug. Particular
CC applications are to determine risk of addiction to opiates or cocaine, or
CC of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in V61984 in
CC accordance with the specification.
XX
SO Sequence 2162 BP; 562 A; 565 C; 457 G; 576 T; 2 other:

```

Query Match 97.0%; Score 1561; DB 19; Length 2162;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

```

Qy 28 TGGGAGGGGCTATAGCAGAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGA 87
Db 1 tgggaagggggctatacagcagaggaatgtcagatgtcctcgtccctccgctga 60
Qy 88 GCGTCTCTCTGCTCAGCCAGAGACTGTTCTGTATAGAAACACAGAGACTGTGCGAGC 147
Db 61 cgcctctctgtctcagcagagctgtttctgttaagaacagcagagctgtgagc 120
Qy 148 GCGCAAGAGAGCGCGTGAAGCGCTTGAACCCGAAAGTCTGCTGCTGCTGCTACT 207
Db 121 ggcgaaggaagcgctgagcgcttgaacccgaaagctcgtgtgtctcctgtact 180

```



```
XX Human mu-opioid receptor cDNA variant 3.
DE
XX
XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KM prediction; addition; analgesic; anaesthetic; anti-addictive;
KM psychopharmacological agent; diagnostic; side effect; drug; opiate;
KM cocaine; inherited alcoholism; human; ss.
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 213..2040
FT CDS
FT
FT /tag- a
FT /product- "mu-opioid receptor"
FT misc-feature 502..503
FT /tag- b
FT /note- "Site of intron 1"
FT misc-feature 855..856
FT /tag- c
FT /note- "Site of intron 2"
FT misc-feature 1376..1377
FT /tag- d
FT /note- "Site of intron 3"
FT mutation 102
FT /tag- e
FT /note- "Wild type C is replaced by T"
XX
XX W0983937-A2.
XX
XX 06-AUG-1998.
XX
XX 02-FEB-1998: 98WC-DE00382.
XX
XX 03-FEB-1997: 97DE-1003925.
XX
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
XX Hoehe M, Wendel B:
XX WPI: 1998-437487/37.
XX
XX New genomic and cDNA sequences encoding human mu-opioid receptor -
XX used, e.g. to predict pre-disposition to addiction and for
XX development of analgesics, anaesthetics and anti-addiction agents
XX
XX
XX Claim 8; Page -: 26pp; German.
XX
XX This sequence encodes a novel human mu-opioid receptor in which a C
XX nucleotide at position 102 of the wild-type sequence represented in
XX CC V61984 is replaced by a T. The wild type receptor and its variants,
XX CC polymorphisms and mutants are used in a method for detecting
XX CC predisposition to disease, particularly addictive disease, by isolating
XX CC DNA from a sample, genotyping selected positions and comparing with a
XX CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
XX CC anti-addictive and psychopharmacological agents, to construct genes and
XX CC vectors, particularly for pharmaceutical development, to develop
XX CC diagnostic kits for predicting risk of addiction, response to analgesics
XX CC or anaesthetics, or development of side effects from a drug. Particular
XX CC applications are to determine risk of addiction to opiates or cocaine, or
XX CC of developing inherited alcoholism.
XX CC Note: This sequence is not represented in the specification and has
XX CC been constructed from the wild-type sequence represented in V61984 in
XX CC accordance with the specification.
XX
XX Sequence 2162 BP: 562 A; 564 C; 458 G; 576 T; 2 other:
SQ
Query Match 97.0% Score 1561; DB 19; Length 2162;
Best Local Similarity 99.6% Pred. No 0;
Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 28 TGGAGGGGGCTATACCGAGAGAGATGTCAGTGTCTAGCTGGTCCCTCGGCTGA 87
```

```
Db 1 tggaggggggctataccgacagaggaatgtcagatgtctcagctcgtccctccgctga 60
QY 88 CGTCTCTCTCTGTCTACGCCAGACGCTGGTTTGTATGAAGAACACGACGAGCTGGCAGC 147
Db 61 cgcctctctcgtctcagccagagactgttctcttgaagaatagcagagactgtgagc 120
QY 148 GGGGAAAGGAAGGGCGTGAGGCGCTTGAACCCGAAAGTCTGGTCTCTGCTGCTACT 207
Db 121 ggcgaagaagagcgctcgaagcgcttggaaacccgaagaagtcctcgtctcgtactc 180
QY 208 CGCACAGC-GTGCCCGCCCGCCGCTCAGTACCATAGGACAGCAGCGCTGCCCGCAGCAG 266
Db 181 cgcacagcgtgtgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 240
QY 267 CCAGCAATTGCACTGATGCTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326
Db 241 ccagcaattgcactgactgactgtcgtactcaagtlgtctcccaagcaccagcccggt 300
QY 327 CCTGGGTCACCTTGTCCACTAGATGGAACCTGTCCGACCCCATGGGTCGGAACCGCA 386
Db 301 cctgggtcaactgtcccaactagatggcaaccgtccgacccatgctcgcgaaccgca 360
QY 387 CCGACCTGGCGGGGAGAGACAGCCTGTGCTCCGACCGGCAAGTCCCTCATGATCAGG 446
Db 361 ccaacctgggggagagagacagcctgtgcctccgacgcgcgcgcgcgcgcgcgcgcgc 420
QY 447 CCATCAGATGATGACCTCTACTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 506
Db 421 ccatacgaatcatagccctcctcactccatcgtgtgtgtgtgtgtgtgtgtgtgtgtgt 480
QY 507 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 566
Db 481 tgtcatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtat 540
QY 567 TCAACCTTGCTGTGGAGATGCTTACCCACCACTACCTGCTTCCAGAGTGTGAATT 626
Db 541 tcaacctgtctgtgcagatgctttagcacaacagctacccgtccctccagtgtagatt 600
QY 627 ACCTAATGGGAAACATGGCCATTTGGAAACATCTTCCAGATGATGATGATGATGATGAT 686
Db 601 accctaattgggaacatgacatltggaaacatcttgcgaagatgtagtccatlaatt 660
QY 687 ACTTAATCATGTTGACAGATATTCACCTCTGACCATGAGTGTGATGATGATGATGATG 746
Db 661 actataacatgttaccagcatatcaccctctgcacacagatgagtggttagcagaaattg 720
QY 747 CAGTGTGCCACCTGTCAAGGCTTAGATTTCGTAATCCCGAAATGCGAAATATATCA 806
Db 721 cagctgtccaaacctgtaagccttagatttcgtactcccgaaatgcgaaatattatca 780
QY 807 ATGTCTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 866
Db 781 atgtctgcaactgtatctctcctcctcctcctcctcctcctcctcctcctcctcctc 840
QY 867 CAATATCAGGCAAGGTTTCCATAGATTGTACACTAATAATTTCTCATCAACCTGCTACT 926
Db 841 caaatacaggaagatgttcatatgattgtacacaaatctctcaccacaaacctgtact 900
QY 927 GGGAAACCTGTGAGATGCTGTGTTTTCATCTTGCTTTCATTATGCAAGTGTCTATCA 986
Db 901 gggaaacctgtgaagatcgtgtttcattcttgcctcattatgtcagtgatcatca 960
QY 987 TTACCGTGTGTATGAGCTATGATCTTGGGCTCAGAGATGTGCCATGCTCTCTGGCT 1046
Db 961 ttaccgtgtgtatgactatgactgtctcgtcccaagagtgctcagatgtctctcgtc 1020
QY 1047 CCAAGAAAGAGACAGAACTTTCGAAGATCACAGAGATGCTGCTGCTGCTGCTGCTGCTG 1106
Db 1021 ccaagaagaaagacagaaatcttcgaagatcacacagaaatggtgtgtgtgtgtgtgtgt 1080
QY 1107 TGTTCATGCTGTGCTGAGCTCCCATTCATTTACGTCATCATTTAAAGCCTTGCTGTTCAA 1166
```

```

Db 1081 tgtcatcgctgctgactccattcacattacatcatcaatgaagccttggtacaa 1140
QY 1167 TCCGAAACTACGTTCCGACTGTTTCTTGACACTTTCGATTTGCTAGGTTACAA 1226
Db 1141 tcccaagaactacgtccagactgttcttgacattcgtcattgctcaggtacaa 1200
QY 1227 ACAGCTGCTCAACCCAGCTTTATGATTTGATGATGATGATGATGATGATGATGAT 1286
Db 1201 acaactgctcacaacccagctcattatgattcttgatgataaactcaacgagcttca 1260
QY 1287 GAGAGTTCTGTATCCCACTCTTCCACATTTGAGCAACAACTCCACTGATTCGTC 1346
Db 1261 gaggagctcgtatcccaactctctccacattgagcaaaaaactccactcgcattcgc 1320
QY 1347 AGAACCTAGAGACCCCTCCAGCGGCCAATACATGATGATGATGATGATGATGATGAT 1406
Db 1321 aagaactagaaacccctccacgccaatacagtgatgataactatcatcagctag 1380
QY 1407 AAAATCTGAGACGAGAACTGCTCCGTTGCTTCAACAGGCTTCATGCGATCCGACTT 1466
Db 1381 aaaaactgaaagaaactgctccgctgcccacaagaggtccatgcatccgacctt 1440
QY 1467 CACCAAGCTTAAAGCCACCATGTATGTGAAACAGGTTGCTTCAAGAAATGTGTAGAG 1526
Db 1441 caaccaagcttagaagccaccatgtagtgaaagcaggttgcctcaagatgtagag 1500
QY 1527 CTCTAATTTCTAGGAAGTGCCTGTTTAACTGATTCACACTCTTCTCTGCGCA 1586
Db 1501 cctaattctcaggaagtgctactttagtgcattcaacctcttctctctgcca 1560
QY 1587 CTCTGCTGACATAGAGG 1607
Db 1561 cctgctcgcacattagag 1581

RESULT 7
V61988
ID V61988 standard; cDNA; 2162 BP.
AC V61988:
XX
DT 11-JAN-1999 (first entry)
DE Human mu-opioid receptor cDNA variant 4.
XX
KM Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW prediopsis; addiction; analgesic; anaesthetic; anti-addictive;
KM psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KM cocaine; inherited alcoholism; human; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 213..2040
FT FT /tag= a
FT FT /product= "mu-opioid receptor"
FT FT /tag= b
FT FT /note= "Site of intron 1"
FT FT 502..503
FT FT /tag= b
FT FT 855..856
FT FT /tag= c
FT FT /note= "Site of intron 2"
FT FT 1376..1377
FT FT /tag= d
FT FT /note= "Site of intron 3"
FT FT 175
FT FT /tag= e
FT FT /note= "Wild type C is replaced by A"
XX
PN WO9833937-A2.
XX
PD 06-AUG-1998.

```

```

XX
PF 02-FEB-1998; 98WO-DE00382.
XX
PR 03-FEB-1997; 97DE-1003925.
XX
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Hoehe M, Wendel B;
XX
DR WPI: 1998-437487/37.
XX
PT New genomic and cDNA sequences encoding human mu-opioid receptor -
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
PS
PS Claim 8, Page -: 26pp; German.
XX
CC This sequence encodes a novel human mu-opioid receptor in which a C
CC nucleotide at position 175 of the wild-type sequence represented in
CC V61984 is replaced by an A. The wild type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC prediopsis to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
CC anti-addictive and psychopharmaceutical agents, to construct genes and
CC vectors, particularly for pharmaceutical development, to develop
CC diagnostic kits for predicting risk of addiction, response to analgesics
CC or anaesthetics, or development of side effects from a drug. Particular
CC applications are to determine risk of addiction to opiates or cocaine, or
CC of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in V61984 in
CC accordance with the specification.
XX
SQ Sequence 2162 BP; 563 A; 564 C; 458 G; 575 T; 2 other:

Query Match 97.0%; Score 1561; DB 19; Length 2162;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 28 TGGAGGGGGCTATACGAGAGAGAAATGTCAGTCTGCTCCCTCCGCTGA 87
Db 1 tgggagggggctatacgcagagagaaatgtagatgtagtgcctccctccgctga 60
QY 88 CGCTCTCTCTGTCTACGACGAGACTGTTTCTGTAAGAAACAGGAGAGCTGTGGACG 147
Db 61 cgctctctctgtctacgcagagactggttctgtaagaacagcagagctgtgcaagc 120
QY 148 GCGGAAGGAGACGGGCTGAGGGCTTGGAAACCCGAAAAGTCTCGGTCTCTGCTACT 207
Db 121 ggcgaaggaagagcgtgtaggcgttgaacccgaaaagctcgtgtcctcgtgatact 180
QY 208 GCGACAGC-GTGCAGCGCCGGCGCTCAGTACATGACAGCGAGCGCTGCGCCCAAGAG 266
Db 181 gcgacagcggtgccccgcgcgtcagtagcatgagcagcgctgcccccaagaag 240
QY 267 CCAGCAATTGACTGATGCTTGGGCTACTCAAGTTGCTCCACAGACCCAGCCGGTT 326
Db 241 ccagcaattgactgactgactgactgactgactgactgactgactgactgactgactg 300
QY 327 CCTGGGTCACTTGTCCCACTTATGATGCAACCTGTCGAGCCATGCGGTCCGAACGCA 386
Db 301 cctgggtcaactgttgcacacttagatggaacactgtccgacacatggtccgaaccga 360
QY 387 CCGACCTGGGCGGAGAGACAGCTGTCCTCCACCGGAGTCCCTCATGATCAGG 446
Db 361 ccaactgggcgagagagacagcctgtgcctccgacccgagctcccatgatacag 420
QY 447 CCATACGATATGCGCCTTACTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 506
Db 421 ccatcagatcagcctcctactcactcactcactcactcactcactcactcactcactc 480

```

Oy	507	TGGTCATATGATGATATTTCTGCATACACAAAGATGAAGACAGCGCACAAACATCTACATTT	566
Db	481	tggctcatatgatagtatgttctgcatacaaccaagaatgaaagactgccaccaacatctacatt	540
Oy	567	TCAACCTTGCTCTGGCAGATGCCCTTAAAGCACAGTACCTGACCCTTCAGAGTGTGAATT	626
Db	541	tcaaccttgctctggcagatgaccttaagccaccagtaaccttgaccttcacagatgtgatt	600
Oy	627	ACCTTAATGGGAACATGGGCATTTTGGAAACATCCTTTGCAAGATAGTATCTCCATAGATT	686
Db	601	accttaatgggaacatgggcatttggaaacatcctttgcaagatagtatctccatagatt	660
Oy	687	ACTAATACATGTCACCGCAGCATATTACACCCCTGACACATAGATGATGGATATACATTG	746
Db	661	actaatacatgtcacccgacatattcacccctgcacacaagaagtgatccacccaacatctac	720
Oy	747	CAGTCTGCCACCCGTGTCAAGGCGCTTAGATTCCGTACTCCCGCAATAGCCAAATATTATCA	806
Db	721	cagtctgccaccctgtcaaggcgttagattccgtactcccgcaatagccaaatattatca	780
Oy	807	ATGTCTGCACACTGGATCTCTCTTCACGCCATGSGTCTTCTGTATGTTCATGGCTACAA	866
Db	781	atgtctgcaactgatactctctcttcacgscattgtctctcgtatattgatagtctacaa	840
Oy	867	CAAAATACAGGCAGGTTCCATACATTTGTATACATACATTCCTGCATCCAAACCTGGTACT	926
Db	841	caaaatacaggcaagggttcatacatattgtatacaacaatcttcctccaccaacccgtgact	900
Oy	927	GGGAAACCTCTGTGAATCTGTGTTTTCATCTTCGCGCTTCATTATTCACAGTGCATCA	986
Db	901	gggaaacctctgtgaagtctgtgttttcattctctgccttcattatgtccagtgctatca	960
Oy	987	TTACCGTGTGCTATGAGACTATATCTTGGCGCTTCAGAGATGTCCGATGCTCTG8GCT	104
Db	961	ttaccgtgtgctatgagactatattcttggcgcttcagagatgtccgatgctctcgtct	1020
Oy	1047	CCAAAGAAAGGACAGGAATCTTGGAAAGATCACAGAGTGTGTCGTG8TGGTGGCTG	110
Db	1021	ccaaagaaaggacaggaaatcttcgaagaacaccagaagaagtcgtagtcgtagtcgtag	108
Oy	1107	TGTTTCATGTCGTGTGACCTGCCATTGCATTTACGTATCATCTTAAAGCCCTGGTTACAA	116
Db	1081	tgttcatgtctgctgtgacacctgccattgcattacgtatcatctttaaagccttggttaca	114
Oy	1167	TCCCAAGAACTACGTTCCAGACTGTTCTTG6CACTTGTGCATGCTCTAG6TTACAAA	122
Db	1141	tcccaagaaactacgtcttcagactgttcttbgcaactctgcatgtcctagttlacaa	120
Oy	1227	ACAGTGGCTCAACCCGATCCTTTATGATTTCTGMAATGMAAATCTMAACGATGCTTCA	128
Db	1201	acagtgctccaacccgattccttlatgattctcgtgataatgcgaactcaaacgattgtcca	126
Oy	1287	GAGAGTTCTGTATCCCAACCTCTTTCACATTTGAGCAAAATCTCAGTCGATTCGTC	134
Db	1261	gagagttctgtatcccaaccttcttlatgattctcgtgataatgcgaactcaaacgattgtcca	126
Oy	1347	AGAACTAGAGACCAACCCCTCCACGCGCAATACAGTGATAGAACTAATCATCAGCTAG	140
Db	1321	agaacactagagaccacccctccacgccaatagacagtgatagaaactaatcatcacgtag	138
Oy	1407	AAATTCGGAAGCAAAATCTCTCCGTTGCCCTTAACAGGGCTCATGCCATTCCGACTT	146
Db	1381	aaatctcggaaagcagaactctctcgttgccttaacagaaggtctctaagttccatccgaactt	144
Oy	1467	CACCAAGGTTTGAAGCCACATGTATGTGGAAGAGAGTGCGTTCAAAATGTGAGGAGG	152
Db	1441	caccaagcttgaagccacacatgtatgtgaagaaggtctctcaagaatcgtatagaagag	150
Oy	1527	CTCTAATTTCTTAGAAAAGTGCCGTGTTTATGATCATCAACCTCTTCTCTGTGGCCA	158
Db	1501	ctctaatctcttagaaagtgctcactttagtgatcatcaaacctcttctctctcgtgcca	156
Oy	1587	CTCTGCTCTGTGCACATTAGAGG 1607	

[illegible]

CC been constructed from the wild-type sequence represented in V61984 in
 CC accordance with the specification.
 XX

Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 2 other;

Query Match 97.0%; Score 1561; DB 19; Length 2162;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

28 TGGGAGGCGGCTATACGACAGAGAAATGTACATGCTCAGCTCGTCCCTCCGCTGA 87
 1 tgggaggggagctatagcagagagaatgtcagatgtctcagctcgtccctccgctga 60
 88 CGCTCTCTCTGTCTACGACGAGACTGTTTCTTAAGAAACAGCAGAGAGCTGTGGCAGC 147
 61 cgtctctctctgtctcagcagagactgttctgttaagaaacagcagagactgtggagc 120
 148 GCGGAAAGAGCGGCTGAGGCGCTTGAACCCGAAAGCTCGTCTGCTGCTACCT 207
 121 ggcgaaagagagcgctgagcgcttgaaaccgaaagctcgtgtctctcgtact 180
 208 CGCACAGC-6TGCCCGCCGCGCGCTCAGTACATGACAGCAGCGCTGCCCGCAGAGC 266
 181 cgcacagcggtgcgcgcgcgctcagtagtaccatgagcagcgctgtcccaagcag 240
 267 CAGGCAATTCAGTACGCTTGGCTTACTCAATGTCTCTCCAGCAGCCAGCCCGCTT 326
 241 cagcaatgactgactgactgtgctgactcaagtgtctcccaagcagcccggt 300
 327 CCTGGGCACTTGTCCCACTAGATGGAACCTGTCCGACCCATGGGCTCGGAGCGCA 386
 301 cctgggcaactgtctccactatgactgactcgtctccgacccatggtgtccgacgca 360
 387 CGCAGCTGGGCGGAGAGACGCTGTGCCCTCCGACCGGAGTCCCTCATGATCAGG 446
 361 ccaactggcgagagagacgctgtgcctccgacgagcagctccatgtagtcag 420
 447 CCATCAGCATATGCGCTTACTCCATCGTGTGCTGTGGGCTTTGGAAACTTCC 506
 421 ccatcagcatatgccccctactccatcgtgtgctgtgggctctcttggaaactcc 480
 507 TGGTCATGTATGTATGTAGATACACAAAGATGAAGACTGCGACCAACATCTACATT 566
 481 tggtcattgtatgtatgtatgatacacaagaatgaaagtgtccacaacatctacatt 540
 567 TCAACCTTGTCTGGCAGATGCTTAGCAGCAGTACCTGCCCTTCAGAGTGTGAATT 626
 541 tcaacctgtctggcagatgcttagcagcagctaccccttcagagtgtagatt 600
 627 ACCTATGGGAATGGCCATTGGAAACATCTTTGCAAGATAGTATCTCCATAGATT 686
 601 acctatgggaatggccatttggaaacatcttttgcagagatgtagtccatagatt 660
 687 ACTATAACATGTTACACAGCATATTACCCCTGACACATGAGTGTGATGATCAATTG 746
 661 actataacatgttaccacagatattccctctgcacacagagtgtgtatcgatacttg 720
 747 CAGTGTGCAACCTGTCAAGGCTTAGATTTCGTACTCCCGCAAAATGCCAAATTAATCA 806
 721 cagtgtgcaacctgtcaaggttagatttccgtactcccgcaaatgcaaaattatca 780
 807 ATGTCTGCAACTGATGATCTCTTACAGCATGTGTCTCTCTGAATGTATGGCTCAA 866
 781 atgtctgcaactgatatctcttccagcatgtgttctctgtatgtatgtatgtataaa 840
 867 CAAATACAGGAGGATTCATAGATGTACATCACTCACTCACTCACTCACTCACTCACT 926
 841 caaatacagagagatgtcatatgtatgtatgtatgtatgtatgtatgtatgtatgtat 900
 927 GGGAAACCTGTGAGAGATGTGTGTTTTCATCTTGGCTTCATTATGCAAGTGTCTATCA 986
 901 gggaacacctgtgagagatgtgtgttttcatcttgccttcattatgtcagtgtagtca 960

987 TTACCGTGTGCTATGAGTATGATGATCTTGCGCTCAAGAGTGTCCGATGCTCTGGCT 1046
 961 ttacggtgtgtatgactgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtat 1020
 1047 CCAAGAAAGAGCAGAGAACTTTCGAAGATCACAGAGATGTGTGTGTGTGTGTGTGTGTGT 1106
 1021 ccaagaaagagcagagaaacttccgaagatcacagagatgtgtgtgtgtgtgtgtgtgtgt 1080
 1107 TGTTCATGCTGTCTGGACTCCCATTCACATTTAGTTCATCATTAAGCCTTGTGTTACAA 1166
 1081 tgttcattgtctgtgtgactcccatccatccattagctcatcatlaaagcctgtgtacaa 1140
 1167 TCCCAAGAAATAGTTCACAGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1226
 1141 tcccaagaaatagttccagactgttctgtgacttctgtcatctgtcatgtgtgtgtacaa 1200
 1227 ACAGCTGCTCAACCCAGTCTTTATGCAATTTGTGATGAAACTTCAACAGATGCTTCA 1286
 1201 acagctgctcaacccagctctttagatcttctgtatgtatgtatgtatgtatgtatgtat 1260
 1287 GAGAGTTCGTATCCCAACCTTTCACATTTAGAGCAACAAATCCACTGGAATTCGTC 1346
 1261 gagagtctgtatcccaacttcccaacatgtagcaacaacaactccactggaattcgtc 1320
 1347 AGAAGACTAGAGACACCCCTCCACGCGCCATACAGTGTGATTAAGTAACTAATCATCAGCTAG 1406
 1321 agaagactagagacacccctccacgcccatacagtgtagtaactaaacatacactag 1380
 1407 AAATCTGAGAGCAGAAAGTCTCCGTTGCCCTTAACAGGCTTCATGCTTCGACCTT 1466
 1381 aaatctgagagcagaaactctcgttgccttccaaaggttccatgcatctcgaactt 1440
 1467 CACCAAGCTTGAAGCCACCATGATGTGAGAGCAGAGTGTCTTCAAGATGTGTAGAGG 1526
 1441 caccaagcttgaagccaccatgtatgtgaagcaggttcttcaagaatgtgtagag 1500
 1527 CTCTAATTCCTTGAAGAGGCTGCTTTAGTCAATCCAACTCTTCTCTCTGCGCA 1586
 1501 ctctaatctcttgaagagagctttagttagtcaacacttctctctcgtgcca 1560
 1587 CTCTGCTCTGACATTAGAGG 1607
 1561 ctctgctctgacattagag 1581

RESULT 9
 ID V61990
 V61990 standard; cDNA; 2162 BP.
 XX
 AC V61990;
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Human mu-opioid receptor cDNA variant 6.
 XX
 KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 KW predisposition; addiction; analgesic; anesthetic; anti-addictive;
 KW psychopharmacological agent; diagnostic; side effect; drug; opiate;
 KW cocaine; inherited alcoholism; human; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX
 FH Key
 FT CDS 213..2040
 FT /tag= a
 FT /product= "mu-opioid receptor"
 FT misc_feature 502..503
 FT /tag= b
 FT /note= "Site of intron 1"
 FT 855..856
 FT misc_feature
 FT /tag= c

FT /note- "Site of intron 2"
 1376..1377
 FT misc_feature
 /tag- d
 FT /note- "Site of intron 3"
 330
 FT mutation
 /*tag- e
 FT /note- "Wild type A is replaced by G"
 MO9833937-A2.
 PN
 XX
 PD 06-AUG-1998.
 XX
 PF 02-FEB-1998; 98MO-DE00382.
 XX
 PR 03-FEB-1997; 97DE-1003925.
 XX
 XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX
 PI Hoehe M, Wendel B;
 XX
 DR WPI; 1998-437487/37.
 XX
 PT New genomic and cDNA sequences encoding human mu-opioid receptor -
 PT used, e.g. to predict pre-disposition to addiction and for
 PT development of analgesics, anaesthetics and anti-addiction agents
 XX
 PS Claim 8: Page -: 26pp; German.
 XX
 CC This sequence encodes a novel human mu-opioid receptor in which an A
 CC nucleotide at position 330 of the wild-type sequence represented in
 CC V61984 is replaced by a G. The wild type receptor and its variants,
 CC polymorphisms and mutants are used in a method for detecting
 CC predisposition to disease, particularly addictive disease, by isolating
 CC DNA from a sample, genotyping selected positions and comparing with a
 CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
 CC anti-addictive and psychopharmaceutical agents, to construct genes and
 CC vectors, particularly for pharmaceutical development, to develop
 CC diagnostic kits for predicting risk of addiction, response to analgesics
 CC or anaesthetics, or development of side effects from a drug. Particular
 CC applications are to determine risk of addiction to opiates or cocaine, or
 CC of developing inherited alcoholism.
 CC Note: This sequence is not represented in the specification and has
 CC been constructed from the wild-type sequence represented in V61984 in
 CC accordance with the specification.
 CC
 XX
 XX Sequence 2162 BP; 561 A; 565 C; 459 G; 575 T; 2 other;
 XX
 Query Match 97.0%; Score 1561; DB 19; Length 2162;
 Best local Similarity 99.6%; Pred. No. 0;
 Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Db 301 cctgggtcaactgtctccactatagatgggagactgtccgaccatcgtgtccgaacgca 360
 QY 387 CCGACCTGGGCGGAGAGAGACAGCCTTGCCCTCCGACCGGCACTCCCTCATGATCAGG 446
 Db 361 ccaacctggcgaggagagaaagccgtgtccctccgacgcaagctccatcatgatacgg 420
 QY 447 CCATCAGATCATGGCCCTACTCATGATGTCGTCGGTGGGGGCTTCGGAACTTCC 506
 Db 421 ccatacagatcagagccctcactccatcgtgtggtggggtccctcgaaacttcc 480
 QY 507 TGGTCATGTAATGTAATGTCAGATACACCAAGATGAAGACTGGCACCAATCTACATT 566
 Db 481 tggatcatgtatgtatgtatgtatgatacacaagaatgaaagactgacacaatcatatt 540
 QY 567 TCAACCTTGCTCTGGCAGATGCTTACGACAGATACCTCGCTTCAGAGTGTGAATT 626
 Db 541 tcaacctgtctcgtgagatgtccttagccacagatccctgccttcagagtgtgaatt 600
 QY 627 ACCTAATGGGACATGGCCATTTGSAACATCCTTTGSAAGATGATTCATGATGATT 686
 Db 601 acctaatgggaaatcagcatttggaaacatcccttgcagaatagatccatcatagatt 660
 QY 687 ACTATACATGTCACACAGATATTCACCTTCGACAGATGATGTTGATCATATTG 746
 Db 661 actatacatgttcacacagcatattcacccctgcacatagtggtgtatcatatcgt 720
 QY 747 CAGTTCGCCACCTGTCAAGGCTTGATTTCCGTACTCCCGAAATGCCAAATATTCA 806
 Db 721 cagctgcacacccctgtcagaagccttagatttcgtactcccgaaatgcgaattatca 780
 QY 807 ATGTGCAACGTGATGATCTCTTCAGCATGTCCTGTCGTAATGTCATGATGATGAT 866
 Db 781 atgtcgcacatcagacccctcctcagccatcgttcttcgtgaatgcagtcacaa 840
 QY 867 CAAATACAGGCAAGGTTCCATGATGATGATGATGATGATGATGATGATGATGATG 926
 Db 841 caaatacagcaaggttccatagattgtacactaatccttccatccaaactgttact 900
 QY 927 GGGAAACCTGCTGAAGATCTGTGTTTTCATCTTCCCTTCATTAAGCAGTCTATA 986
 Db 901 gggaaacctcgtgaaagactgtgtttcatcttcgtcccttcaatgacagtgctatca 960
 QY 987 TTACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1046
 Db 961 ttacgtgtcatgtgactgactgactgtcgtcctcaagatgttcgcagatcctcgtgt 1020
 QY 1047 CAAAGAAAAAGACAGAAATCTTGAAGATCACAGATGTCGTGTGTGTGTGTGTG 1106
 Db 1021 ccaagaagaagcaggaatcttcgaagatccacagatgtgtgtgtgtgtgtgtgtgt 1080
 QY 1107 TGTTCATGCTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1166
 Db 1081 tgttcacgtcgtcgt 1140
 QY 1167 TCCCAAAATACAGTTCAGAGATGTTTGTGCACTTTCGACTTTCAGTGTGATACAA 1226
 Db 1141 tcccagaactaactgtccagactgtttcttgcgaacttcgcgaatgtccagtttaca 1200
 QY 1227 ACAAGTGCCTCAACCCAGTCTTTATGATTTCTGATGAAAACTTCAAAAGATGCTT 1295
 Db 1201 acagcgtcctcaacccagtccttaltgacttctgtatgaataactcaagaatgttca 1260
 QY 1287 GAGAGTTGTATCCCAACCTTTCGAATGATGAGACAAAACTCCACTCGAATTCGT 1346
 Db 1261 gagagttcgttaccacactcttccaaacttgagaaactcaactcatcgaattcgtc 1320
 QY 1347 AGAACACTAGAGACCCCTCCAGGCAATACAGTGTGATGATGATGATGATGATGAT 1406
 Db 1321 agaaactagagacacccctccacagccaaatacaagtgatgaactaatcatcagctg 1380
 QY 1407 AAATCTGGAAGAGAAATGCTGCTGCTGCTTAACAGGATGATGATGATGATGATGAT 1466

DR WPI: 1998-437487/37.
XX New genomic and cDNA sequences encoding human mu-opioid receptor -
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
XX
PS Claim 8; Page -: 26pp; German.
XX
CC This sequence encodes a novel human mu-opioid receptor in which a T
CC nucleotide at position 1014 of the wild-type sequence represented in
CC V61984 is replaced by a C. The wild type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
CC anti-addictive and psychopharmaceutical agents, to construct genes and
CC vectors, particularly for pharmaceutical development, to develop
CC diagnostic kits for predicting risk of addiction, response to analgesics
CC or anaesthetics, or development of side effects from a drug. Particular
CC applications are to determine risk of addiction to opiates or cocaine, or
CC of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in V61984 in
CC accordance with the specification.
CC
XX
SQ Sequence 2162 BP; 562 A; 566 C; 458 G; 574 T; 2 other:

- Query Match 97.0%; Score 1561; DB 19; Length 2162;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 28 TGGGAGGGGCTATACGAGAGAGAGATGTCAGATGTCAGTCCGCTCCCTGCA 87
DB 1 tgggaaggggctatacagcagaggaagatgcatgctcagctcgtctccctcgccga 60
QY 88 CGCTCTCTCTGTCTACGCCAGGACTGGTTCTGTGAAGAACAGAGAGAGCTGTGGACG 147
DB 61 cgtctctctctctcagccagagactggttctgtgaagaaacagagagagctgtgcaagc 120
QY 148 GGGCAAGAGAGCGGCTGAGCGGCTTGGACCCGAAAGTCTCGGTGCTCTGCTGCTACT 207
DB 121 ggcgaagaaagagcgctgagcgcttggaacccgaagatcgcgtctcctggtactac 180
QY 208 CGCAGAGC-GTGCCGCGCGCGGCTGACATGACATGAGCAGCAGCCTGCCCGACGAAAG 266
DB 181 cgcacagagcggtccgcgcgcgcgtcagtaacatgagcagcagcgctgcccccaagacg 240
QY 267 CGAGCAATGCACTGATGCTTGGCGTACTCAAGTTGCTCCCGACACCCAGCCGGGT 326
DB 241 ccagcaatgcatgcatgcttgcgtgactcaagtgctcccgagcaccagccccggtt 300
QY 327 CCTGGGTCAATTTGTCACCTTAAGTGGCAACTGTCCGACCCAGCGCGTCCGAACCGCA 386
DB 301 cctgggtcaactgtcccaactagaatgcaacctgtccgaccatgcygtccgaacgca 360
QY 387 CCGAGCTGGGGGAGAGACAGCCTGTGCTCCGACCGGAGTCCCTCCATGATCAGG 446
DB 361 ccaactcgggggagagagacagcctgtgctcctccgacccgagctccctccatgacaagg 420
QY 447 CCATCAGCATATGAGCCCTTACTCCATGCTGTGCGTGTGGGGCTTTCGAAACTTCC 506
DB 421 ccatacagatcatgagccctctactccatcgtgctggtgggtctcttcgaaactcc 480
QY 507 TGGTCATGATGATGATTTTCAGATACACAGATGAAGACATGACCAATCTCATTT 566
DB 481 tggatcatgatagtatgtatgtacatacacaagatgaagactgccaacatctcaatct 540
QY 567 TCAACCTGCTCTGAGAGATGCTTACGACACAGATGCTGCTTCCAGATGTAAT 626
DB 541 tcaacctgtcctcgtcagatgctccttagcaccagtaacctgctccatcagatgtgtaatt 600
QY 627 ACCTAATGGAAACATGGCCATTTGGAACCATCTTTGCAAGATGATGATTCATGATT 686

DB 601 acctaatggaacatgagccattgaaacacatctcttgaaagatagtgatcccatagatt 660
QY 687 ACTATACATGTTTACCCAGCATATTCACCTCTGACATAGTGTGATGATACATG 746
DB 661 actataacatgttcaaccagcatatccacctctgcacatgagtgatgtatcatatctt 720
QY 747 CAGTCTGCCACCTGTCAAGGCTTAGATTGCTGCTACTCCCGGAAATCCAAATATCA 806
DB 721 cagctgtcacccgtctcaagccttagatttcgctactccccgaatgcaaatatca 780
QY 807 ATGTCTGCAATGGATCTCTCTTACGCAATGGCTTCTGTATGTTCATGCTACAA 866
DB 781 atgtctgaactgtgactctctctccacgcatgtgtctcgtaatgttcatgtctacaa 840
QY 867 CAAATACAGCAAGGCTCCATATGATGATACATGATGATGATGATGATGATGATGAT 926
DB 841 caaatatacagcaaggttccatagatgttatacctaacaatctctcatccaacccgttact 900
QY 927 GGGAAACCTGTCAGATGCTGTGTTTCATCTTTCGCTTCATATGCAAGTGCATCA 986
DB 901 gggaaacactctgtgaagatcgtgttttcatcttcgcctcatatgccaagtgtcatca 960
QY 987 TTACGTGTGCTATGAGATGATGATCTTGGCTCAAGAGTGTCCGATGCTGTGCT 1046
DB 961 ttacgtgtgtatgactgtatgtatcttgcgtcccaagatgtccgactgtccctgct 1020
QY 1047 CCAAGAAAGAGACAGAAATTTGAAAGATCACAGATGCTGCTGCTGCTGCTG 1106
DB 1021 ccaagaaagaaagaaagaaatcttcgaagaaacacaaagatgtgtgtgtgtgtgtgt 1080
QY 1107 TGTTCATGCTGTGCTGAGCTGCTCCATTCATGATGATGATGATGATGATGATGATGAT 1166
DB 1081 tgttcattgtctgtgtgactccatccatcttcaatctgtcatcatataaagcctgtttaca 1140
QY 1167 TCCAGAAACTAGCTTCCAGACTGTTTCTGTGGCACTTGTGCTGCTGCTGCTGCTGCT 1226
DB 1141 tccagaaactagcttccagactgttcttctgtgcaactctgtcatgtcttgaattacaa 1200
QY 1227 ACAGTGTGCTCAACCGACTGCTTATGATGATGATGATGATGATGATGATGATGATGAT 1286
DB 1201 acaagtgtcttaacccagctcccttcatgtatcttcgagatgaaacttcaacagatgttca 1260
QY 1287 GAGAGTCTGTATCCCAACCTCTTCCAACTTGAAGATGAGCAACAACTCCAGTATGCTG 1346
DB 1261 gagagtctgtatcccaacctcttccaaatgtgagcaaaactccaatcgaattgtctc 1320
QY 1347 AGAAGCTAGAGACACCCCTCCACGGCCAAATACAGTGAATGAATATCATCAGCTAG 1406
DB 1321 agaacactagagacacccctccacgccaatatacagatgataactaatcatagctag 1380
QY 1407 AAAATCTGAGAGCAAACTGCTCGTTGGCTTAACAGGGGCTCATGCGATTCGACCTT 1466
DB 1381 aaatctggaagagaaactgtccgtgtgcccatacagggctctatgccaatccgacctt 1440
QY 1467 CACCAAGCTTAGAAGCCACCATGTATGTGAAGCAGGTGCTTCAAGATGTGAAGAG 1526
DB 1441 cacaagcttagaagccaacctgtatgtggaagcaggttgttcaagaatgtgtagaagg 1500
QY 1527 CTCTAATTTCTAGAAAGTGCCTTTTATGATCAACATCTTTCTCTGTGCGCA 1586
DB 1501 ctctaatctcttagaagatgtcctacttttagtcatccaacctcttctctctgtgcca 1560
QY 1587 CTCTGCTCTGCACTTAGAGG 1607
DB 1561 ctctgctctgcaacttagaag 1581

RESULT 13
V61994
ID V61994 standard; cDNA: 2162 BP.
XX
AC V61994;

QY	875	AGCAAGGTCATAGATTGTACACTAACATTCTCTCATCCAACTGGTACTGGGAAAC	934
Db	849	aggcaaggctccatagatctgtacacaaacatctctccacacctggtaactgggaaac	908
QY	935	CTGCAGGATGTGTGTTTTCATCTCCGCTTCATTATGCGCAGTGCATCATTAACGGTG	994
Db	905	cccggaagatctggtttccatctctgcctccatctaaagcagtgctcatctaacctg	968
QY	995	TGCTATGACTGATGATCTTGCGCCTCAAGAGTGTCCGCATGCTCTGTGAGCCAAAGAA	1054
Db	969	tgcctatgacgtatgatctctgtgcctccaaaggtgctcgcatgctctctgtgtccaaagaa	1028
QY	1055	AAGGACAGGAATCTTTCGAAAGATACACAGGATGGTGTGTGTGTGTGTGTGTATC	1114
Db	1029	aaggacaggaaatctctcgaaggatccacccggatggtgtgtgtgtgtgtgtgtgtgtc	1088
QY	1115	GACTCTGGACTCCCATTCACATTTACGTACATCATTAAGGCTGGTACAACTCCAGAA	1174
Db	1089	gctgtctgtgactcccatccatccatcttaagtcattcatctaaagccttggttacaatccagaa	1148
QY	1175	ACTACGTTCCAGACTGTGTTCTTTGGCATTCTGCATTGCTCTAGGTTACAAACAGCTGC	1234
Db	1149	actaagctccagactgctttcttcttggaactctgcattgtcttaggttacaacacagctgc	1208
QY	1235	CTCACCACAGTCTCTTATGACTTTCTGGATGAAAACTTCAACGATGCTTACAGAGCTTC	1294
Db	1209	ctcaaccagatcccttatactgtcatcttctgtatgtaaaacttcaacagatgtcttaagagatlc	1268
QY	1295	TGTATCCCAACTCTTCTCCACACTTGAGCAGCAAAACTCCACTCGAATTCGTACAGACT	1354
Db	1269	tgtatcccaactcctctccaacatgtagaagcaaaaaactccatctgaattcgtccagaacact	1328
QY	1335	AGAGACCAACCCCTCCAGGCGCCATACAGTGGATAGACTAATCATCAGCTGAAAAATCTG	1414
Db	1329	agaagaccacccctccacagcgcacatcacagttagaactaatcatcacagtagaanaatctg	1388
QY	1415	GAAGCAGAAACTGCTCGCTTGCCCTTAACAGGTCATACGCAATCCGACCTTTCACCAAGC	1474
Db	1389	gaagcaagaacatgctccgtgcgtcccaagaaggtccatgacatctccgctccacaaagc	1448
QY	1475	TTAGAAGCCACCATGTATGTGGAAACAGAGTGTCTTCAAGATGTGTAGAGAGGCTCTAAT	1534
Db	1449	ttagaagcacacatgtatagtgaagcaggtgtctccaagaatgtgtatggagagcttaatt	1508
QY	1535	CTCTAGGAAAGTGCTGCTTTTAGGTCAATCCAACCTTTTCTCTGTGGCCACTCTGCTC	1594
Db	1509	ctctaggaagatgctactcttttaggtcatcaacctcttctctctctgycacactgtctc	1568
QY	1595	TGCACATTAGAGG 1607	
Db	1569	tgcacattagaag 1581	
RESULT 15			
ID	288470		
XX	288470	standard; DNA: 2162 BP.	
XX	AC	288470:	
XX	XX	11-MAY-2000 (first entry)	
XX	DE	Human mu opioid receptor gene.	
XX	DE		
KW	KW	Human; mu opioid receptor; hMOR1; diagnosis; addiction; constipation;	
KW	KW	diarrhoea; decreased immune response; stress; gastrointestinal motility;	
KW	KW	immune response; hypothalamus pituitary adrenal axis; gonadal axis;	
KW	KW	pain; opioid; cocaine; nicotine; barbiturate; sedative hypnotic;	
KW	KW	antioxytic; alcohol; ds.	
XX	XX	Homo sapiens.	
XX	XX		
XX	XX	WO200003024-A2.	

[illegible]

OY 335 AACTGTGTCCCACTTAGATGGCAACCTGTCCGACCCATCGGTCCGAAACCGCACCACTTG 394
 Db aactgtgtcccaacttagatggaacactgtccgaaccacatggttcggaacgcacaaacttg 368
 OY 395 GGGGGGAGAGACAGCTGTGCCCCCGACCGGACATGCTCCCTTCATGATCAAGGCCATACAG 454
 Db ggcggaagagacagcctgtgccctccgacgagcagctccctccatgatcaagcgcatacg 428
 OY 455 ATCATGGGCCCTCTACTCCATCGTGTGGGTGTGGGGGCTCTTGGGAACTTCCTGGTCATG 514
 Db atcatgggccctctactccatcgttgtgcgttggttggtcttcggaactctccgcatcg 488
 OY 515 TATGTGATTGTCCAGTACACCAAGATGAAGCTGCCCAACAATCTCATTTTCAACTT 574

QY	1415	GAAGCAGAAATGCTCCGTGCTCCCTTAACAGGGCTCATCCATTCCGACCTTACCAACG	1474
Db	1389	gaacgacgaaaactgctccgttcggtccctcaagggctcatccattccgacctcaccaagc	1448
QY	1475	TTAGAGCCACATGTAATGTGGAAGAGGTTGGCTTCAAGATGTGAGAGGCTTAAT	1534
Db	1449	ttagaagccaccatgctctggaagaaggttgccttaagaatggtgaaagagctctaatt	1508
QY	1535	CTTAGGAAATGGCTCTCTTTTAGGTATCAACAACCTTTCTCTCTGAGCACTCTGTC	1594
Db	1509	ctctagaagaagtgcctactatttagtgcattccaaccccttctcctctcgccacctctgctc	1568
QY	1595	TGCACATTGAAGG	1607
Db	1569	tgccacattgaag	1581

Search completed: November 14, 2000, 22:45:11
Job time: 8511 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2000, 19:12:11 : Search time 838.13 Seconds

(without alignments)
11876.819 Million cell updates/sec

Title: US-08-305-518-7

Perfect score: 1610
Sequence: 1 CGGATGAGCCTCTGTGACT.....GCTCTGCACATTAGAGCCG 1610

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
27: gb_est27:*
28: gb_est28:*
29: gb_est29:*
30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: em_estda:*
42: em_estfun:*
43: em_esthum1:*

44: em_esthum2:*
45: em_esthum3:*
46: em_esthum4:*
47: em_esthum5:*
48: em_esthum6:*
49: em_esthum7:*
50: em_esthum8:*
51: em_esthum9:*
52: em_esthum10:*
53: em_esthum11:*
54: em_esthum12:*
55: em_esthum13:*
56: em_esthum14:*
57: em_esthum15:*
58: em_esthum16:*
59: em_esthum17:*
60: em_esthum18:*
61: em_esthum19:*
62: em_esthum20:*
63: em_estin1:*
64: em_estin2:*
65: em_estin3:*
66: em_estin4:*
67: em_estom:*
68: em_estov1:*
69: em_estov2:*
70: em_estp11:*
71: em_estp12:*
72: em_estp13:*
73: em_estp14:*
74: em_estp15:*
75: em_estro1:*
76: em_estro2:*
77: em_estro3:*
78: em_estro4:*
79: em_estro5:*
80: em_estro6:*
81: em_estro7:*
82: em_estro8:*
83: em_estro9:*
84: em_estro10:*
85: em_estro11:*
86: em_estro12:*
87: em_estro13:*
88: gb_gss1:*
89: gb_gss2:*
90: gb_gss3:*
91: gb_gss4:*
92: em_gss1:*
93: em_gss2:*
94: em_gss3:*
95: em_gss4:*
96: gb_gss5:*
97: gb_gss6:*
98: gb_gss7:*
99: gb_gss8:*
100: gb_gss9:*
101: gb_gss10:*
102: gb_gss11:*
103: gb_gss12:*
104: gb_gss13:*
105: gb_gss14:*
106: gb_gss15:*
107: gb_gss16:*
108: gb_gss17:*
109: gb_gss18:*
110: gb_gss19:*
111: gb_gss20:*
112: gb_gss21:*
113: gb_gss22:*
114: gb_gss23:*
115: gb_gss24:*
116: em_gss5:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	323.6	20.1	520	B82759	B82759, RPCI11-17K2
C 2	322.2	20.0	1053	CNS04C2T	AL283934 Tetradon
C 3	227	14.1	525	AQ767579	AQ767579 HS_3206_A
C 4	213.8	13.3	836	CNS02261	AL177778 Tetradon
C 5	211	13.1	877	CNS02SC2	AL211691 Tetradon
C 6	191	11.9	842	CNS02SCU	AL212007 Tetradon
C 7	186.8	11.6	710	CNS012MG	AL174481 Tetradon
C 8	184.2	11.4	433	AM489031	AM489031 UT-M-BH3-
C 9	158.6	9.9	927	CNS04RP2	AL304175 Tetradon
C 10	158.2	9.8	881	CNS03JCN	AM373832 OV3-BT053
C 11	155.4	9.7	654	AM373832	AM373832 OV3-BT053
C 12	137.6	8.5	427	AM047705	AM047705 UT-M-BH1-
C 13	136.4	8.5	245	AQ486720	AQ486720 RPCI11-17K2
C 14	130.4	8.1	642	BE252309	BE252309 601114162
C 15	124	7.7	546	AZ226406	AZ226406 RPCI1-23-8
C 16	123.8	7.7	937	CNS03GSG	AL243385 Tetradon
C 17	117.2	7.3	193	CNS04ROE	AL304223 Tetradon
C 18	115.4	7.2	188	R81583	R81583 Y104B04.r1
C 19	112.2	7.0	638	AM919332	AM919332 EST350636
C 20	108	6.7	656	AL119185	AL119185 DRP7P.61N
C 21	107.2	6.7	534	AM652898	AM652898 101337 MA
C 22	98.2	6.1	794	CNS01WC1	AL110218 Tetradon
C 23	92.6	5.8	992	CNS02ZGZ	AL221605 Tetradon
C 24	90.8	5.6	844	CNS03CLX	AL237966 Tetradon
C 25	89	5.5	153	R31984	R31984 yb62c10.r1
C 26	80.4	5.0	901	CNS01SK5	AL165326 Tetradon
C 27	79	4.9	1029	CNS03SOZ	AL258812 Tetradon
C 28	72.4	4.5	552	AJ393659	AJ393659 AJ393659
C 29	71.2	4.4	640	BE198338	BE198338 uc77d12.Y
C 30	70.8	4.4	543	AM516933	AM516933 xq04a06.x
C 31	70	4.3	817	CNS03DJV	AL229260 Tetradon
C 32	69	4.3	378	CNS03HHA	AL244747 Tetradon
C 33	68.8	4.3	557	AM669715	AM669715 113242 MA
C 34	68.4	4.2	595	AA940565	AA940565 vz4606.r
C 35	68.2	4.2	1002	CNS02CMB	AL117922 Tetradon
C 36	66.8	4.1	529	AM653917	AM653917 102840 MA
C 37	66.6	4.1	485	BE128304	BE128304 DEPA2054
C 38	66.2	4.1	485	AM453011	AM453011 UT-H-BM1-
C 39	66.2	4.1	530	AM028270	AM028270 wv86b03.x
C 40	66.2	4.1	738	AL1475600	AL1475600 tc92h03.Y
C 41	65.8	4.1	592	AL048512	AL048512 DRP2P586M
C 42	65.6	4.1	866	CNS02RML	AL210810 Tetradon
C 43	65.4	4.1	391	N93987	N93987 2a66d09.r1
C 44	65.4	4.0	932	CNS02STR	AL211932 Tetradon
C 45	64.2	4.0	434	AI263529	AI263529 q120c06.x

ALIGNMENTS

RESULT 1
B82759/c

LOCUS B82759 520 bp DNA GSS 09-APR-1999
DEFINITION RPCI11-17K2.TP RPCI11 Homo sapiens genomic clone RPCI11-17K22,
DNA sequence.
ACCESSION B82759
VERSION B82759.1 GI:2869782
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 520)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.
TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: RPCI11-17K22.TVB
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: madams@tigr.org
Clones are derived from the human BAC library RPCI11. For BAC
library availability, please contact Pieter de Jong
(pieter@jeong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES

SOURCE
1..520
/organism="Homo sapiens"
/db_xref="GDB:7506405"
/db_xref="taxon:9606"
/clone="RPCI11-17K22"
/clone_id="RPCI11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC library"
BASE COUNT 101 a 154 c 153 g 112 t
ORIGIN

Query Match 20.1% Score 323.6; DB 111; Length 520;
Best Local Similarity 97.1% Pred. No. 3.2e-85;
Matches 340; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

OY 190 CGGTCCTGCTGCTACCTCGCACAGC-GTGGCCGGCCGGCGGTAGTACATGACACACA 248
|||||
DB 520 CGGTCCTGCTGCTACCTCGCACAGC-GTGGCCGGCCGGCGGTAGTACATGACACACA 461
|||||
OY 249 GCGCTGCCCGCCAGCAGCAGCAATTCAGTATGCTTGGCTACTCAAGTTGCTCC 308
|||||
DB 460 GCGCTGCCCGCCAGCAGCAGCAATTCAGTATGCTTGGCTACTCAAGTTGCTCC 401
|||||
OY 309 CAGCAGCCAGCCCGGTTCTGGGTCAACTGTCCCACTTAGATGAGCAACTGTCCGAC 368
|||||
DB 400 CAGCAGCCAGCAGCGTTCTGGGTCAACTGTCCCACTTAGATGAGCAACTGTCCGAC 341
|||||
OY 369 CATGGGTCCGACCGCAGCAGCAGCTGGGGGGAGAGACAGCTGGCCCTCGACCGGCA 428
|||||
DB 340 CATGGGTCCGACCGCAGCAGCAGCTGGGGGGAGAGACAGCTGGCCCTCGACCGGCA 281
|||||
OY 429 GTCCCTCATGATACAGGCATACAGATGAGCCCTTACTCATCTGCTGCTGAG 488
|||||
DB 280 GTCCCTCATGATACAGGCATACAGATGAGCCCTTACTCATCTGCTGCTGAG 221
|||||
OY 489 GGCCTTCGGAACCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 111
|||||

BAC end Web Server: <http://www.htsc.washington.edu>

Plate: 3206 row: 1 column: 9

Seq primer: T7

Class: BAC ends

High quality sequence stop: 525.

FEATURES

source

Location/Qualifiers

1..525

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_id="CIT Approved Human Genomic Sperm Library D"

/sex="male"

/note="Organ: sperm; Vector: pBelOBAC11; BAC clones in E-Coli DH10B"

BASE COUNT

ORIGIN

123 a

139 c

126 g

133 t

4 others

Query Match

Best Local Similarity

81.4%;

Score 227;

DB 102;

Length 525;

Pred. No. 1.9e-56;

Mismatches 263;

Conservative 0;

Mismatches 60;

Indels 0;

Gaps 0;

Matches 263;

Conservative 0;

Mismatches 60;

Indels 0;

Gaps 0;

Matches 263;

Conservative 0;

Mismatches 60;

Indels 0;

Gaps 0;

Matches 263;

Conservative 0;

Mismatches 60;

Indels 0;

Gaps 0;

Matches 263;

Conservative 0;

Mismatches 60;

Indels 0;

Gaps 0;

Matches 263;

Conservative 0;

Mismatches 60;

Indels 0;

Gaps 0;

TITLE
Saurin, W. and Weissenbach, J.
Human genome number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

REFERENCE
Unpublished
3 (bases 1 to 836)

AUTHORS
Genoscope.

TITLE
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

JOURNAL
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at

COMMENT
<http://www.genoscope.cns.fr/tetraodon>.

FEATURES

source

Location/Qualifiers

1..836

/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"

/clone_id="227103"

/note="Genoscope sequence ID : C0AG227AE02UP1-end : T7"

BASE COUNT

ORIGIN

190 a

240 c

203 g

197 t

6 others

Query Match

Best Local Similarity

75.4%;

Score 213.8;

DB 113;

Length 836;

Pred. No. 2e-52;

Mismatches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches 266;

Conservative 0;

Mismatches 87;

Indels 0;

Gaps 0;

Matches

freshwater pufferfish Tetraodon nigroviridis

REFERENCE 2 (bases 1 to 877)
 AUTHORS Roest-Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brotlier, P., Quetier, F., Saurin, W. and Weissenbach, J.
 TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 877)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
 COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.
 FEATURES
 source 1..877
 /organism="Tetraodon nigroviridis"
 /db_xref="taxon:99883"
 /clone_1lb="G"
 /note="Genoscope sequence ID : C0AG161D03SP1-end : PUC-ORI"

BASE COUNT 201 a 249 c 214 g 197 t 16 others

ORIGIN

Query Match 13.1%; Score 211; DB 113; Length 877;
 Best Local Similarity 74.2%; Pred. No. 1.4e-51;
 Matches 262; Conservative 3; Mismatches 88; Indels 0; Gaps 0;

QY 527 AGATACCAAGATGAAGACTGCCACACATCTACATTTTCAACCTTGTCTGGCAGAT 586
 |||||||
 DB 348 AGGTACACCAAGATGAAGACCGCCACMACATCTACATTTTCAACCTTGTCTGGCAGAC 407
 |||||||
 QY 587 GCCTTGCCCAAGTACCCCGCCCTTCCAGAGTGTGATTAATGGAACATGGSCCA 646
 |||||||
 DB 408 GCTTGACCCACGACACCTCCCTTCCAGAGGCGCAAGTACCTGATGAACAGTGTGCG 467
 |||||||
 QY 647 TTGGAACCATCTTTGCAAGATGATGATCCATAGATTACTATAACATGTTACACAGC 706
 |||||||
 DB 468 TTGGGGAGAGTGTGTAACAGTGTGATGCGCATGACATCAACAAGTGTGACACAGC 527
 |||||||
 QY 707 ATATTACCTCTGCAACATGATGATGATGATGATGATGATGATGATGATGATGATG 766
 |||||||
 DB 528 ATCTTACGCTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 587
 |||||||
 QY 767 GCCTTGATTTGCTGCTACTCCGCAAAATGCAAAATTAATCAATGTCGCAACGTGATCCTC 826
 |||||||
 DB 588 GCGCTGAGCTTCCGACACCCGCCAAGGCCAATATCAATCAATGTTGATCTGATCTC 647
 |||||||
 QY 827 TCTTCAGCAATGCTCTCTGTAATGTTGATGCTACAAACAATAACAGCA 879
 |||||||
 DB 648 TCTTCAGCGGTGGAGTACCCGATGATGATGATGATGATGATGATGATGATGATGATG 700
 |||||||

RESULT 6
 CDS02SKU/c 842 bp DNA GSS 15-MAY-2000
 LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
 DEFINITION 16218 of library G from Tetraodon nigroviridis, genomic survey
 sequence.
 ACCESSION AL212007.1 GI:7870826
 VERSION AL212007.1
 KEYWORDS GSS; genome survey sequence.
 SOURCE Tetraodon nigroviridis.
 ORGANISM Tetraodon nigroviridis.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
 Holacanthopterygii; Acanthopterygii; Percomorpha;

Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 842)
 AUTHORS Roest-Crolius, H., Jallion, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
 TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 842)
 AUTHORS Roest-Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brotlier, P., Quetier, F., Saurin, W. and Weissenbach, J.
 TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 842)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
 COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.
 FEATURES
 source 1..842
 /organism="Tetraodon nigroviridis"
 /db_xref="taxon:99883"
 /clone_1lb="G"
 /note="Genoscope sequence ID : C0AG162BC09LP1-end : T7"

BASE COUNT 135 a 272 c 285 g 141 t 9 others

ORIGIN

Query Match 11.9%; Score 191; DB 113; Length 842;
 Best Local Similarity 62.2%; Pred. No. 1.2e-45;
 Matches 306; Conservative 6; Mismatches 177; Indels 3; Gaps 1;

QY 888 TAGATGTACATACATCTCTATCCAACTGGTACTGAGAAACCTGCTGAATCT 947
 |||||
 DB 781 TGTGTGCGCGCTGACATTCGCCGACCGCGCTGCTGAGGACCGCTCAATCT 722
 |||||
 QY 948 GTGTTTCATCTGCGCTTCATATGCGAGTGTGATGATGATGATGATGATGATGATG 1007
 |||||
 DB 721 GCGTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 662
 |||||
 QY 1008 TGAATTTGCGCCCTCAAGAGTGTCCGATGCTCTGCTGCTCAAAAGAAAGAGAGATC 1067
 |||||
 DB 661 TGAATCTGCGCGCTGAGAGAGTGTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCA 602
 |||||
 QY 1068 TTGAAGATACACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1127
 |||||
 DB 601 GCGCGCGCATACCCGCAAGGGGCTGTGTGTGCGCGCGCTGCTGCTGCTGCTGCTGCT 542
 |||||
 QY 1128 CCAATTCATTTGATGATCATTAAGCTTGTGATTAAGCTTGTGATTAAGCTTGTGATTA 1184
 |||||
 DB 541 CCAATTCATCTCATCAAGGGGAGAGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAG 482
 |||||
 QY 1185 AGACTGTTCTGGCACTTCTGATGCTCTAGATTACAAACAGCTGCTCAACCCAG 1244
 |||||
 DB 481 TGTGTGCGCGCTGCGACCTGCGATGCGCTGCGCAACCAACAGACAGCTCAACCCGC 422
 |||||
 QY 1245 TCGTTTATGATTTCTGATGAAACTTAAACGATGCTTCAAGAGTCTGATGCCAA 1304
 |||||
 DB 421 TCTTCAGCGCTTCTGCGAGAGAACTCAAGAGGCTTCCGGGATTCCTGCTCTCCCT 362
 |||||
 QY 1305 CCCTTCCAAATTTGCAACAAACTCCACTGCAATTCAGAAACATTAAGAGACACC 1364
 |||||
 DB 361 GCGGAGCGCGAGCG 302
 |||||
 QY 1365 CCTTCAAGGCCA 1376
 |||||
 DB 301 CCTCCTCGCA 290
 |||||


```

RESULT 7
CNS012MG/C 710 bp DNA GSS 12-MAY-2000
LOCUS Tetradon nigroviridis genome survey sequence PUC-0r1 end of clone
DEFINITION 220N19 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION AL174481 GI:7812538
KEYWORDS GSS: genome survey sequence.
SOURCE Tetradon nigroviridis.
ORGANISM Tetradon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Eucanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorphi;
Tetraodontiformes; Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 710)
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,
Bonneau,L., Billault,A., Quetier,F., Saulin,W., Bernot,A. and
Weissenbach,J.
JOURNAL Characterization and repeat analysis of the compact genome of the
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 710)
Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,
Bonneau,L., Billault,A., Quetier,F., Saulin,W., Bernot,A.,
Sautin,M. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 710)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
1..710
location/Qualifiers
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="220N19"
/clone_11b="G"
/note="Genoscope sequence ID : C0AG220CG10SP1-end :
PUC-0r1"
BASE COUNT 134 a 152 c 216 g 191 t 17 others
ORIGIN
Query Match 11 6%; Score 186.8; DB 113; Length 710;
Best Local Similarity 72.0%; Pred. No. 2e-44; Indels 1; Gaps 1;
Matches 247; Conservative 6; Mismatches 89;

```

```

Db 265 AAGCGGTGACCTTACAGGACCGCCGACCAAGCAAGATATCTCAACGTCYCAACTGATTC 206
QY 825 TCTCTTACGACCATGTGCTCTTCTGTATATGTTCATGGCTCAAC 867
Db 205 TGTCCCGCCGACGATGCGACTTCAGTCATGTCTGCTCCAC 163
RESULT 8
AM489031/C 433 bp mRNA EST 24-FEB-2000
LOCUS UI-M-BH3-ssd-d-09-0-UI.s1 NIH_BMAP_M.S4 Mus musculus cDNA clone
DEFINITION UI-M-BH3-ssd-d-09-0-UI 3', mRNA sequence.
ACCESSION AM489031
VERSION AM489031.1 GI:7059301
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 433)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
JOURNAL Normalization and subtraction: two approaches to facilitate gene
REFERENCE discovery
AUTHORS Genome Res. 6 (9), 791-806 (1996)
JOURNAL 97044477
COMMENT Contact: Chn, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov
Oligo-6T track not found, Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
Seq primer: M13 forward
POLYA-No.
FEATURES
source
1..433
location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH3-ssd-d-09-0-UI"
/clone_11b="NIH_BMAP_M.S4"
/dev_stage="27-32 days"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M.S4 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stem, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hippocampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: NIH_BMAP_M.S4,
NIH_BMAP_M.S3.3, NIH_BMAP_M.S3.2, NIH_BMAP_M.S3.1,
NIH_BMAP_M.S2, NIH_BMAP_M.S1. The subtracted library
(NIH_BMAP_M.S4) was constructed as follows: PCR amplified
cDNA inserts from NIH_BMAP_M.S3.3, NIH_BMAP_M.S3.2, and
NIH_BMAP_M.S3.1 clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M.S3.3, NIH_BMAP_M.S3.2, and NIH_BMAP_M.S3.1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated

```

into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldi, Lennon and Soares, Genome Research

TITLE Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

JOURNAL Unpublished
REFERENCE 3 (bases 1 to 881)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/tetradon>.

FEATURES
source
1. 881
/organism="Tetradon nigroviridis"
/db_xref="taxon:99883"
/clone_1lb="G"
/clone_1lb="G"
/note="Genoscope sequence ID : COBG031AB1LP1-end : T7"

BASE COUNT 202 a 212 c 236 g 231 t

ORIGIN

Query Match 9.8%; Score 158.2; DB 114; Length 881;
Best Local Similarity 76.4%; Pred. No. 7.4e-36;
Matches 207; Conservative 0; Mismatches 63; Indels 1; Gaps 1;

525 TCAGATACCAAGATAGAGCTGCGACCAACATCTACATTTGACCTGCTGCGAG 584
|||||
270 TTAGTACCAAAATAGAGCGGCACAAACATCTACATTTGACCTGCGCG 211
|||||
585 ATGCTAGGACAGATGACCTGCTGCGAGAGTGAATTAATGGAATGCG 644
|||||
210 AGCGCTGTCACAGAGACGCTTCCCTTCAGAGCGTCACTACCTGATGGCG 151
|||||
645 CATTTGACCAATCTTTCAGAGATGATCTCATAGATTAATTAACATGTCACCA 704
|||||
150 C-TTCGCGAGAGCTGCTGCGAGATCTCATGCTCACTACCAACATGTTCACT 92
|||||
705 GCATATCACACCTGACCATGATGTTGATGATCATGATGAGTGGACACCTGCA 764
|||||
91 CCATCTTACAGCTACCAACATGAGCTGAGCGCTGAGCGTGTGCGATCGGATCA 32
|||||
765 AGGCTTATGATTTCCGCTACTCCCGGAATGC 795
|||||
31 AAGGCTGAGACTTCAGAGCGCGCAACGC 1
|||||

RESULT 11
AM373832
LOCUS AM373832 654 bp mRNA
DEFINITION QV3-BT0537-221299-048-h10 BT0537 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM373832
VERSION AM373832.1 GI:6878486
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 654)
HGCP <http://www.ludwig.org.br/ORESTES>.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV3&t2-QV3-BT0537->

221299-048-h10&t3=1999-12-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 639.
Location/Qualifiers
1. 654
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="BT0537"
/dev_stage="Adult"
/note="Organ: Breast; Vector: puc18; Site:1: Sma1; Site:2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 117 a 210 c 185 g 142 t

ORIGIN

Query Match 9.7%; Score 155.4; DB 21; Length 654;
Best Local Similarity 68.9%; Pred. No. 4.5e-35;
Matches 213; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

450 TCAGATCATGACCCCTCTACTCCATGCTGCGTGGGAGCTTCGAACTTCCTGG 509
|||||
346 TCACATCTGTCGGGCTCTACTGCGCTGTGTGTGCGAGGAGCTTCGGAACTGCTTG 405
|||||
510 TCATGATGATGATTCAGATACCAAGATGAAGACTGCGACCAATCTACATTTTCA 569
|||||
406 TCATGATGATGATTCAGATACCAAGATGAAGACTGCGACCAATCTACATTTTCA 465
|||||
570 ACCTTGCTGCGAGATGCTTGAACCAAGTACCTGCGCTTCGAGAGTGAATTAC 629
|||||
466 ACCTGCGCTGCGAGACTGCTGCTGCTGAGCTGCGCTTCGAGGCGACGACATCC 525
|||||
630 TAATGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 689
|||||
526 TCCTGCGCTTCTGCGCTGCGGATGCGCTGTGCAAGACATGATGATGATGATGATGAT 585
|||||
690 ATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 749
|||||
586 ACAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 645
|||||
750 TCTGCCACC 758
|||||
646 TCTGCCACC 654
|||||

RESULT 12
AM047705/c
LOCUS AM047705/c 427 bp mRNA
DEFINITION UI-M-BH1-a10-f-04-0-UI-s1 NIH-BMAP-M-S2 Mus musculus cDNA clone
UI-M-BH1-a10-f-04-0-UI 3', mRNA sequence.
ACCESSION AM047705
VERSION AM047705.1 GI:5908234
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 427)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
JOURNAL Contact: Chin, H
COMMENT National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2000, 21:43:02 ; Search time 1824.62 Seconds

(without alignments)
3853.845 Million cell updates/sec

Title: US-08-305-518-7

Perfect score: 1610
Sequence: 1 CCGATGAGCGCTGTGACT.....GCTCTGACATTAGAGCCG 1610

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1033670 seqs, 2183789903 residues

Word size : 35

Total number of hits satisfying chosen parameters: 43

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:*

1: gb_bal:*

2: gb_bal2:*

3: gb_om:*

4: gb_ov:*

5: gb_pat:*

6: gb_ph:*

7: gb_pl1:*

8: gb_pl2:*

9: gb_pl1:*

10: gb_pl2:*

11: gb_pl3:*

12: gb_ro:*

13: gb_sy:*

14: gb_un:*

15: em_fun:*

16: em_hum1:*

17: em_hum2:*

18: em_in:*

19: em_om:*

20: em_or:*

21: em_ov:*

22: em_pat:*

23: em_ph:*

24: em_pl:*

25: em_ro:*

26: em_sts:*

27: em_sy:*

28: em_un:*

29: em_vl:*

30: gb_bal3:*

31: gb_in1:*

32: gb_in2:*

33: gb_in3:*

34: gb_pl3:*

35: gb_pl4:*

36: em_bal:*

37: em_bal2:*

38: em_hgt1:*

39: em_hgt2:*

40: em_hgt3:*

41: em_hgt4:*

42: em_hgt5:*

43: em_hgt6:*

44: em_hgt7:*

45: em_hgt8:*

46: em_hgt9:*

47: em_hgt10:*

48: em_hgt11:*

49: em_hgt12:*

50: em_hgt13:*

51: em_hgt14:*

52: em_hgt15:*

53: em_hgt16:*

54: em_hgt17:*

55: em_hgt18:*

56: em_hgt19:*

57: em_hgt20:*

58: em_hgt21:*

59: em_hgt22:*

60: em_hgt23:*

61: em_hum3:*

62: em_hum4:*

63: em_hum5:*

64: em_hum6:*

65: gb_pr5:*

66: gb_pr6:*

67: gb_pr7:*

68: gb_hgt1:*

69: gb_hgt2:*

70: gb_hgt3:*

71: gb_hgt4:*

72: gb_hgt5:*

73: gb_hgt6:*

74: gb_hgt7:*

75: gb_hgt8:*

76: gb_hgt9:*

77: gb_hgt10:*

78: gb_hgt11:*

79: gb_hgt12:*

80: gb_hgt13:*

81: gb_hgt14:*

82: gb_hgt15:*

83: gb_hgt16:*

84: gb_hgt17:*

85: gb_hgt18:*

86: gb_hgt19:*

87: gb_hgt20:*

88: gb_hgt21:*

89: gb_hgt22:*

90: gb_hgt23:*

91: gb_sts1:*

92: gb_sts2:*

93: gb_vl1:*

94: gb_vl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1610	100.0	1610	67	HUMOPTIOIDA	L29301 Homo sapien
2	1236	78.0	2162	5	A87781	A87781 Sequence 7
3	1240	77.0	2162	67	HUMMOR1X	L25119 Human Mu op
4	1086	67.5	1473	66	HSU12569	U12569 Human mu op
5	523	32.5	124569	88	AL359850	AL359850 Homo sapi
6	523	32.5	131426	85	AL136444	AL136444 Homo sapi
7	487	30.2	1598	66	HSOPRMT2	AF024516 Homo sapi
8	406	25.2	124569	88	AL359850	AL359850 Homo sapi
9	406	25.2	182048	80	AC027439	AC027439 Homo sapi
10	406	25.2	182383	75	AC021745	AC021745 Homo sapi
11	357	22.2	182048	80	AC027439	AC027439 Homo sapi
12	267	16.5	1203	11	AF286024	AF286024 Macaca mu

13	251	15.6	305	66	HSOPRM1	AF024515 Homo sapi
14	215	13.4	3759	11	AF153500	Homo sapi
15	209	13.0	98104	66	HSJ402L9	AL132774 Human DNA
16	207	12.9	530	91	G53082	SHGC-84785
17	141	8.8	233	11	AF100548	Macaca mu
18	115	7.1	400	91	G11298	human STS S
19	115	7.1	400	91	G13228	human STS U
20	112	7.0	669	66	HSOPRM3	AF024517 Homo sapi
21	74	4.6	1415	3	BT089677	Bos taurus
22	74	4.6	17313	76	AC022855	Homo sapi
23	71	4.4	1881	3	P1GM0PR	AC022855 Homo sapi
24	59	3.7	371	12	MM0R2	L38645 Sus scrofa
25	59	3.7	1334	12	AF074973	Mus muscu
26	59	3.7	1423	12	AF062753	Mus muscu
27	59	3.7	1543	12	AF074974	Mus muscu
28	59	3.7	1610	12	MM026915	Mus muscu
29	59	3.7	1729	12	AF167568	Mus muscu
30	59	3.7	2229	5	A68824	Sequence 1
31	59	3.7	2229	12	MM019380	Mus muscu
32	59	3.7	178454	81	AC055776	Mus muscu
33	50	3.1	193	3	AF266480	Ovis arie
34	49	3.0	77313	76	AC022855	Homo sapi
35	47	2.9	1367	12	RN035424	Rattus norv
36	47	2.9	1401	12	RATMOP10D	L22455 Ratt mu opio
37	47	2.9	1448	12	RN02083	Rattus norv
38	47	2.9	1586	12	RATMORA	L13069 Rattus norv
39	47	2.9	2135	12	RATMORA	L10684 Rattus norv
40	47	2.9	2397	12	RATRORE	D16349 Rat mRNA fo
41	41	2.5	720	12	S77863	mu-opioid r
42	38	2.4	354	12	CP067928	Cavala porce
43	35	2.2	1944	12	S79903	mu opioid r

ALIGNMENTS

RESULT 1
LOCUS HUMOPI01DA 1610 bp mRNA PRI
DEFINITION Homo sapiens opiod receptor mRNA, complete cds.
ACCESSION L29301
VERSION L29301.1 GI:459831
KEYWORDS opiod receptor.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1610)
AUTHORS Westek, A., Hurley, J.H., Bye, L.S., Campbell, A.D., Chen, Y., Tian, M., Liu, J., Schulman, H. and Yu, L.
TITLE The human mu opiod receptor: modulation of functional desensitization by calcium/calmodulin-dependent protein kinase and protein kinase C

JOURNAL J Neurosci. 15 (3), 2396-2406 (1995)
MEDLINE 95198115

FEATURES
source Location/Qualifiers

CDS

1..1610
/organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_stage="adult"
/tissue_type="caudate nucleus"
/tissue_lib="Clontech lambda gt11"
239..1441
/note="putative"
/codon_start=1
/product="opiod receptor"
/protein_id="AA073958.1"
/db_xref="GI:459832"
/translation="MDSNAAPTNASNCTDALAYSSGSPAPSPGWNLSHLDNLSDP
CGPNRDLGGDSLCEPTGSPNITATITIALYSIVCYVGLGNFLVYVIYRTKM
TATNTYFNLALADALATSTLPGSYNVMGTWMPGTILCKIVISIDYNNMTSFTL
CTMSYDRIYAVCHPYKALDFRTPRNKTIINVCNWIISAGLPEVPMATTKRQSDIN
CLTFPSHTWMLNKLKICVFIFAFIMPLIITVCCGLMLILKLSKVRMLSGSKERDN

BASE COUNT 384 a 467 c 359 g 400 t

ORIGIN

Query Match 100.0%; Score 1610; DB 67; Length 1610;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGATGAGCCCTGTGTAAGTGAAGTGGAGGGGCTTACGACAGAGATGTCAG 60
1 CGATGAGCCCTGTGTAAGTGAAGTGGAGGGGCTTACGACAGAGATGTCAG 60
61 ATGTGAGCTGCGTCCCTCGCTGACGCTCTCTGTGTCAGCAGACAGCTTCT 120
61 ATGTGAGCTGCGTCCCTCGCTGACGCTCTCTGTGTCAGCAGACAGCTTCT 120
61 ATGTGAGCTGCGTCCCTCGCTGACGCTCTCTGTGTCAGCAGACAGCTTCT 120
121 GTAAGAAACAGCAGAGCTGTGGCAGCGGGAAGAGAGGGGCTTGAACCC 180
121 GTAAGAAACAGCAGAGCTGTGGCAGCGGGAAGAGAGGGGCTTGAACCC 180
181 GAAAGTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
181 GAAAGTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
241 GGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
241 GGACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
301 TTGCTCCCGCAGCAGCCAGCCCGGCTTCTGCTGCTGCTGCTGCTGCTGCT 360
301 TTGCTCCCGCAGCAGCCAGCCCGGCTTCTGCTGCTGCTGCTGCTGCTGCT 360
361 GTCCGACCATGCGGTCGCAACCGACCGACCTGGGGGGAGAGACGCTGCTCC 420
361 GTCCGACCATGCGGTCGCAACCGACCGACCTGGGGGGAGAGACGCTGCTCC 420
421 GACCGGAGTCCCTCATGATGATGATGATGATGATGATGATGATGATGATG 480
421 GACCGGAGTCCCTCATGATGATGATGATGATGATGATGATGATGATGATG 480
481 CGTGTGGGCTCTTGGGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
481 CGTGTGGGCTCTTGGGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
541 GAAGACTGCGCAGACATCTTCACTTTTCACTTTTCACTTTTCACTTTTCA 600
541 GAAGACTGCGCAGACATCTTCACTTTTCACTTTTCACTTTTCACTTTTCA 600
601 TACCTGCGCTTCCAGAGTGAATTAATTAATTAATTAATTAATTAATTAAT 660
601 TACCTGCGCTTCCAGAGTGAATTAATTAATTAATTAATTAATTAATTAAT 660
661 TTGCAAGATAGTATCTCATATAGTATAGTATAGTATAGTATAGTATAGTAT 720
661 TTGCAAGATAGTATCTCATATAGTATAGTATAGTATAGTATAGTATAGTAT 720
721 CACCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
721 CACCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
781 TACTCCCGGAAATGCAAAATTAATTAATTAATTAATTAATTAATTAATTA 840
781 TACTCCCGGAAATGCAAAATTAATTAATTAATTAATTAATTAATTAATTA 840
841 TCTCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
841 TCTCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
901 AACATCTCATCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
901 AACATCTCATCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960

Db 901 AACATTCCTCATCCACCTGGTACTGGGAAACCTGCTGAAGATCTGTGTTTCACTT 960
 QY 961 CGCCTTCATTAAGCAGTGTCTATCATTAACCTGTGCTATGAGCTGATATCTTGGCCT 1020
 Db 961 CGCCTTCATTAAGCAGTGTCTATCATTAACCTGTGCTATGAGCTGATATCTTGGCCT 1020
 QY 1021 CAGAGTGTCCGATGCTCTGTGGCTCCAAAGAAAGAGAGAAATCTTGAAGATCAC 1080
 Db 1021 CAGAGTGTCCGATGCTCTGTGGCTCCAAAGAAAGAGAGAAATCTTGAAGATCAC 1080
 QY 1081 CAGAGTGTGCTGT 1140
 Db 1081 CAGAGTGTGCTGT 1140
 QY 1141 CGTCTCATTAAGCAGT 1200
 Db 1141 CGTCTCATTAAGCAGT 1200
 QY 1201 CTTGTGATGCTGT 1260
 Db 1201 CTTGTGATGCTGT 1260
 QY 1261 GGATGATAAATCTTAAACGATGCTTGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
 Db 1261 GGATGATAAATCTTAAACGATGCTTGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
 QY 1321 GCAACAAAACCTCCATTCGATTCGACAGACCTAGAGCCACCCCTCCAGGCGCAATAC 1380
 Db 1321 GCAACAAAACCTCCATTCGATTCGACAGACCTAGAGCCACCCCTCCAGGCGCAATAC 1380
 QY 1381 AGTGTATGAATCAATCATCATCTGAGAAATCTGGAAGAGAAAGTGTGTGTGTGTGTGT 1440
 Db 1381 AGTGTATGAATCAATCATCATCTGAGAAATCTGGAAGAGAAAGTGTGTGTGTGTGTGT 1440
 QY 1441 ACAGGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 Db 1441 ACAGGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 QY 1501 AGTGTGCTTCAAGATGT 1560
 Db 1501 AGTGTGCTTCAAGATGT 1560
 QY 1561 CATCAACCTCTTCT 1610
 Db 1561 CATCAACCTCTTCT 1610

RESULT 2
 A87781 2162 bp DNA PAT 22-JAN-2000
 LOCUS A87781
 DEFINITION Sequence 7 from Patent WO9833937.
 ACCESSION A87781
 VERSION A87781.1 GI:6736383
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 2162)
 AUTHORS Hoehe, M. and Wendel, B.
 TITLE GENOMIC SEQUENCE OF THE HUMAN mu -OPIOID RECEPTOR GENE AND THE
 VARIANTS, POLYMORPHISMS AND MUTATIONS THEREOF
 JOURNAL Patent: WO 9833937-A 06-AUG-1998;
 HOEHE MARGRET (DE); WENDEL BIRGIT (DE)
 FEATURES
 source 1..2162
 /organism="unidentified"
 /db_xref="taxon:32644"
 BASE COUNT 562 a 565 c 458 g 575 t 2 others
 ORIGIN

Query Match 78.0%; Score 1256; DB 5; length 2162;
 Best Local Similarity 99.7%; Pred. No. 0;

Matches 1576; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 QY 28 TGGGAGGGGGCTATACGAGAGAGAAATGTCAAGTGTCTGAGTGGTCCCTCCGCTGA 87
 Db 1 TGGGAGGGGGCTATACGAGAGAGAAATGTCAAGTGTCTGAGTGGTCCCTCCGCTGA 50
 QY 88 CGCT 147
 Db 61 CGCT 120
 QY 148 GCGGAAAGAGAGCGGCTGAGGCGCTTGGAAACCCGAAAGTCTCGTGTCTGCTTACT 207
 Db 121 GCGGAAAGAGAGCGGCTGAGGCGCTTGGAAACCCGAAAGTCTCGTGTCTGCTTACT 180
 QY 208 GCGACAGC-GTGCCCGCGCGCGCTGAGTACCAGTGGAGAGAGCGCTGCGCCAGGAAC 266
 Db 181 GCGACAGGAGTGTGCCCGCGCGCGCTGAGTACCAGTGGAGAGAGCGCTGCGCCAGGAAC 240
 QY 267 CCAGCAATTTGACATGATGCTGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326
 Db 241 CCAGCAATTTGACATGATGCTGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 QY 327 CCGGAGTCAACTGTGCCACTTGAATGAGCAACCTGTCCGACCATGCGGTCGGAACGCA 386
 Db 301 CCGGAGTCAACTGTGCCACTTGAATGAGCAACCTGTCCGACCATGCGGTCGGAACGCA 360
 QY 387 CCGAGCTGGGGGGGAG 446
 Db 361 CCGAGCTGGGGGGGAG 420
 QY 447 CCATACAGATCATGAGCCCT 506
 Db 421 CCATACAGATCATGAGCCCT 480
 QY 507 TGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 566
 Db 481 TGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 QY 567 TCAACCTTGTCTGTGCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 626
 Db 541 TCAACCTTGTCTGTGCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
 QY 627 ACCATATGGAAACATGGGCAATTTGGAAACATCTTGGAAATAGTATCTTCATAGATT 686
 Db 601 ACCATATGGAAACATGGGCAATTTGGAAACATCTTGGAAATAGTATCTTCATAGATT 660
 QY 687 ACTATACATGTTTCAACAGCATATTCACCTCTGCAACCATGAGTGTGATGATGATGATG 746
 Db 661 ACTATACATGTTTCAACAGCATATTCACCTCTGCAACCATGAGTGTGATGATGATGATG 720
 QY 747 CAGTCTGCCACCCGTGTCAAGGCTTGAATTTCCGTACTGCCGAAATGCAAAATTTATCA 806
 Db 721 CAGTCTGCCACCCGTGTCAAGGCTTGAATTTCCGTACTGCCGAAATGCAAAATTTATCA 780
 QY 807 ATGTCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 866
 Db 781 ATGTCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 867 CAAATATACAGGAGAGGATTCATAGATGATGATGATGATGATGATGATGATGATGATGAT 926
 Db 841 CAAATATACAGGAGAGGATTCATAGATGATGATGATGATGATGATGATGATGATGATGAT 900
 QY 927 GGGAAACCTCTGTGAAGATGT 985
 Db 901 GGGAAACCTCTGTGAAGATGT 960
 QY 987 TTACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1046
 Db 961 TTACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
 QY 1047 CCAAGAAAGAGAGAGATCTTGAAGATTCACAGAGATGATGATGATGATGATGATGATG 1106
 Db 1021 CCAAGAAAGAGAGAGATCTTGAAGATTCACAGAGATGATGATGATGATGATGATGATG 1080

1107 TGTTCATGTCGTGGAGTCCCATTCACATTTAGCATCATTAAGCCTTGTTACAA 1166
1081 TGTTCATGTCGTGGAGTCCCATTCACATTTAGCATCATTAAGCCTTGTTACAA 1140
1167 TCCCGAAGACTAGTTCAGACTGTTTCTGGCACTTTCATGCTAGTTCAGTTCACAA 1226
1141 TCCCGAAGACTAGTTCAGACTGTTTCTGGCACTTTCATGCTAGTTCAGTTCACAA 1200
1227 ACAGTTCGCTCAACCCAGTCCCTTTATGCTATTCGATTAAGCAAACTTCAGTTCCTCA 1286
1201 ACAGTTCGCTCAACCCAGTCCCTTTATGCTATTCGATTAAGCAAACTTCAGTTCCTCA 1260
1287 GAGAGTTCGCTCAACCCAGTCCCTTTATGCTATTCGATTAAGCAAACTTCAGTTCCTCA 1346
1261 GAGAGTTCGCTCAACCCAGTCCCTTTATGCTATTCGATTAAGCAAACTTCAGTTCCTCA 1320
1347 AGAAGACTAGAGACACCCCTCCAGGCGCAATACAGTGTAGAACTAATCATCAGCTAG 1406
1321 AGAAGACTAGAGACACCCCTCCAGGCGCAATACAGTGTAGAACTAATCATCAGCTAG 1380
1407 AAAATCTGGAGACAAACTGCTCCGTTGCCCTAACAGGGTCTCATGCCATTCCGACCTT 1466
1381 AAAATCTGGAGACAAACTGCTCCGTTGCCCTAACAGGGTCTCATGCCATTCCGACCTT 1440
1467 CACCAAGCTTAGAGACACCATGATATGTGAGCAGGTGCTTCAAGATGTGTAGAGAG 1526
1441 CACCAAGCTTAGAGACACCATGATATGTGAGCAGGTGCTTCAAGATGTGTAGAGAG 1500
1527 CTCTAATCTCTAGAAAGTGCCTCTTTAGGTCATCCACCTCTTCTCTGAGCCA 1586
1501 CTCTAATCTCTAGAAAGTGCCTCTTTAGGTCATCCACCTCTTCTCTGAGCCA 1560
1587 CTCTGCTCTGCAATTAGAG 1607
1561 CTCTGCTCTGCAATTAGAG 1581

RESULT 3
HUMMORIX 2162 bp mRNA PRI 08-AUG-1994
DEFINITION Human Mu opiate receptor (MOR1) mRNA, complete cds.
ACCESSION L25119
VERSION L25119.1 GI:452072
KEYWORDS Mu opiate receptor.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2162)
AUTHORS Wang,J.B., Johnson,P.S., Persico,A.M., Hawkins,A.L., Griffin,C.A.
and Uhl,G.R.
TITLE Human mu opiate receptor. cDNA and genomic clones. pharmacologic
characterization and chromosomal assignment
JOURNAL FEBS Lett. 338 (2), 217-222 (1994)
MEDLINE 94139928
FEATURES
source location/Qualifiers
1..2162
/organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_stage="adult"
/tissue_1lb="lambda ZAP; Stratagene"
213..1415
/gene="MOR1"
213..1415
/gene="MOR1"
/codon_start=1
/product="Mu opiate receptor"
/protein_id="AAA20580.1"
/db_xref="GI:452073"
/translation="MDSAAATNNSNCIDALAYSSCPSPGSMVNLSHDGLSDP
CGPRINIGRDSICPPGSPSMITATITMLISIVCVGFGNFWVTVVTRTKK
TAINIYIFNLADALATSTLPQSVNLTMGTPGPIILCKIVISIDYNNMTSIFTL

BASE COUNT 563 a 566 c 455 g 576 t 2 others
ORIGIN
CTMSVDRIAVCHPALKALDEFTPEPNNAKILNVCMWILSSAIGLPVMEATTKYRGSLD
CTLSESHPTVMNENLVKICVFIFAFIEPVLITVCYGLMLRLKSVMLSGSKEDLN
LRTRERLVVAVNATVYCMPIRHYVILKATVETPTPTQVSHPCIALGYNLSCLN
PVILAFIDENFKRFREFCIPFTSSNIDQNSTRIQNTROHPSIANTVDKTHQLENL
EAETAPLP"
Query Match 77.08; Score 1240; DB 67; Length 2162;
Best Local Similarity 99.78; Pred. No. 0;
Matches 1560; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
44 GCAGAGGAGAAATGTCAGATGCTACAGTCCCTCCGCTGAGCTCTCTGTCTC 103
17 GCAGAGGAGAAATGTCAGATGCTACAGTCCCTCCGCTGAGCTCTCTGTCTC 76
104 AGCCAGACTGATTTCTGTAAAGAAACAGCAGAGAGCTGTGCGAGCGGCGAAGAGCGGC 163
77 AGCCAGACTGATTTCTGTAAAGAAACAGCAGAGAGCTGTGCGAGCGGCGAAGAGCGGC 136
164 TGAGGCGCTTGGAACCCGAAAGTCTCGGTCTCTGTCTACCTTGCACAGC -GTGCCG 222
137 TGAGGCGCTTGGAACCCGAAAGTCTCGGTCTCTGTCTACCTTGCACAGCAGGTCGCCG 196
223 CCGGCGCTTGGAACCCGAAAGTCTCGGTCTCTGTCTACCTTGCACAGCAGGTCGCCG 282
197 CCGGCGCTTGGAACCCGAAAGTCTCGGTCTCTGTCTACCTTGCACAGCAGGTCGCCG 256
283 TGCCCTTGCGTACTCAAGTCTCTCCGACGACGACGCGCGGTCTCGGTCAACTGTTC 342
257 TGCCCTTGCGTACTCAAGTCTCTCCGACGACGACGCGCGGTCTCGGTCAACTGTTC 316
343 CCACCTAATGTCGAACCTGTCCGACCCATGGGTCGCCAAGCGGCGGCGGAG 402
317 CCACCTAATGTCGAACCTGTCCGACCCATGGGTCGCCAAGCGGCGGCGGAG 376
403 AGACAGCCTGTGCCCTCCGACCGGAGTCCCTCCATGATGTCAGGCGCATCAGATCATGGC 462
377 AGACAGCCTGTGCCCTCCGACCGGAGTCCCTCCATGATGTCAGGCGCATCAGATCATGGC 436
463 CCTCTCTCCATCGTGTGCGGTGGGCTCTTGGAAACTCTCTGTCATGATGTAT 522
437 CCTCTCTCCATCGTGTGCGGTGGGCTCTTGGAAACTCTCTGTCATGATGTAT 496
523 TGTGATACACCAAGATGAGAGCTGCCACCAATCTACATTTCAACCTGTGCTGGC 582
497 TGTGATACACCAAGATGAGAGCTGCCACCAATCTACATTTCAACCTGTGCTGGC 556
583 AGATGCTTACGCAACAGATGAGAGCTGCCACCAATCTACATTTCAACCTGTGCTGGC 642
557 AGATGCTTACGCAACAGATGAGAGCTGCCACCAATCTACATTTCAACCTGTGCTGGC 616
643 GCCATTGGAACCATCTCTTCCAAAGATGTGATCTCCATTAATTAATCAATGTTTAC 702
617 GCCATTGGAACCATCTCTTCCAAAGATGTGATCTCCATTAATTAATCAATGTTTAC 676
703 CAGCATTTACCCCTGTGACATGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 762
677 CAGCATTTACCCCTGTGACATGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 736
763 CAGGCGCTTAATTTCCCTTACCCCGAAGTCCGAAATTAATTAATTAATGTTTACCTGAT 822
737 CAGGCGCTTAATTTCCCTTACCCCGAAGTCCGAAATTAATTAATTAATGTTTACCTGAT 796
823 CCTCTCTACGCAATGTGTCTCTGTATATGATGATGATGATGATGATGATGATGATGATGAT 892
797 CCTCTCTACGCAATGTGTCTCTGTATATGATGATGATGATGATGATGATGATGATGATGAT 856
883 TTCCATTAATTTGACATTAATTTCTCATCAACCGGATGATGATGATGATGATGATGATGAT 942
857 TTCCATTAATTTGACATTAATTTCTCATCAACCGGATGATGATGATGATGATGATGATGAT 916

* 17030 21195: contig of 4166 bp in length
* 21196 21295: gap of 100 bp in length
* 22348 22547: contig of 1252 bp in length
* 22648 22647: gap of 100 bp in length
* 22648 28063: contig of 5416 bp in length
* 28064 28163: gap of 100 bp in length
* 28164 30406: contig of 2243 bp in length
* 30407 30506: gap of 100 bp in length
* 30507 32053: contig of 1547 bp in length
* 32054 32153: gap of 100 bp in length
* 32154 34236: contig of 2083 bp in length
* 34237 34336: gap of 100 bp in length
* 34337 36558: contig of 2222 bp in length
* 36559 36658: gap of 100 bp in length
* 36659 38408: contig of 1750 bp in length
* 38409 38508: gap of 100 bp in length
* 38509 40660: contig of 2152 bp in length
* 40661 40760: gap of 100 bp in length
* 40761 42115: contig of 1355 bp in length
* 42116 42215: gap of 100 bp in length
* 42216 45404: contig of 3189 bp in length
* 45405 45504: gap of 100 bp in length
* 45505 47767: contig of 2263 bp in length
* 47768 47867: gap of 100 bp in length
* 47868 50333: contig of 2466 bp in length
* 50334 50433: gap of 100 bp in length
* 50434 53910: contig of 3477 bp in length
* 53911 54010: gap of 100 bp in length
* 54011 55124: contig of 1114 bp in length
* 55125 55224: gap of 100 bp in length
* 55225 57215: contig of 1991 bp in length
* 57216 57315: gap of 100 bp in length
* 57316 58382: contig of 1067 bp in length
* 58383 58482: gap of 100 bp in length
* 58483 80755: contig of 22273 bp in length
* 80756 80855: gap of 100 bp in length
* 80856 81866: contig of 1011 bp in length
* 81867 81966: gap of 100 bp in length
* 81967 85210: contig of 3244 bp in length
* 85211 85310: gap of 100 bp in length
* 85311 87074: contig of 1764 bp in length
* 87075 87174: gap of 100 bp in length
* 87175 91511: contig of 4337 bp in length
* 91512 91611: gap of 100 bp in length
* 91612 92650: contig of 1039 bp in length
* 92651 92750: gap of 100 bp in length
* 92751 95618: contig of 2868 bp in length
* 95619 95718: gap of 100 bp in length
* 95719 97558: contig of 1840 bp in length
* 97559 97658: gap of 100 bp in length
* 97659 100174: contig of 2516 bp in length
* 100175 100274: gap of 100 bp in length
* 100275 101789: contig of 1515 bp in length
* 101790 101889: gap of 100 bp in length
* 101890 103053: contig of 1164 bp in length
* 103054 103153: gap of 100 bp in length
* 103154 106517: contig of 3364 bp in length
* 106518 106617: gap of 100 bp in length
* 106618 107662: contig of 1045 bp in length
* 107663 107762: gap of 100 bp in length
* 107763 110688: contig of 2926 bp in length
* 110689 110788: gap of 100 bp in length
* 110789 115340: contig of 4552 bp in length
* 115341 115440: gap of 100 bp in length
* 115441 124569: contig of 9129 bp in length.

FEATURES

source

1. 124569

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="6"

/clone="RP11-157M8"

/clone_lib="RPc1-11.1"

misc_feature

1. 1459

misc_feature /note="assembly_fragment:01001
fragment_chain:1"
1560..3320
/note="assembly_fragment:00995
fragment_chain:1"
3421..5562
/note="assembly_fragment:00697
fragment_chain:1"
5663..9774
/note="assembly_fragment:01147
fragment_chain:1"
9875..11521
/note="assembly_fragment:00015
fragment_chain:2"
11622..14784
/note="assembly_fragment:01088
fragment_chain:2"
14885..16929
/note="assembly_fragment:01190
fragment_chain:2"
17030..21195
/note="assembly_fragment:00007
fragment_chain:3"
21296..22547
/note="assembly_fragment:00142
fragment_chain:3"
22648..28063
/note="assembly_fragment:00116
fragment_chain:4"
28164..30406
/note="assembly_fragment:01178
fragment_chain:4"
30507..32053
/note="assembly_fragment:00512
fragment_chain:5"
32154..34236
/note="assembly_fragment:00924
fragment_chain:5"
34337..36558
/note="assembly_fragment:00743
fragment_chain:6"
36659..38408
/note="assembly_fragment:00187
fragment_chain:6"
38509..40660
/note="assembly_fragment:00749
fragment_chain:7"
40761..42115
/note="assembly_fragment:00794
fragment_chain:7"
42216..45404
/note="assembly_fragment:01106
fragment_chain:8"
45505..47767
/note="assembly_fragment:00346
fragment_chain:8"
47868..50333
/note="assembly_fragment:00023"
50434..53910
/note="assembly_fragment:00085"
54011..55124
/note="assembly_fragment:00099"
55225..57215
/note="assembly_fragment:00139"
57316..58382
/note="assembly_fragment:00161"
58483..80755
/note="assembly_fragment:00266"
80856..81866

Query Match 32.5%; Score 523; DB 88; Length 124569;
Best Local Similarity 100.0%; Pred. No. 3e-287;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 880 AGGTTCCATAGATTGTACACTATCTCTCATCCCACTGGAGTGGGAAACCTGCT 939
 |||||||
 Db 54492 AGGTTCCATAGATTGTACACTATCTCTCATCCCACTGGAGTGGGAAACCTGCT 54551
 QY 940 GAAGATCTGTGTTTTCATCTTCCCTTCATTAAGCAGTGCATATACCGTGTGCTA 999
 |||||||
 Db 54552 GAAGATCTGTGTTTTCATCTTCCCTTCATTAAGCAGTGCATATACCGTGTGCTA 54611
 QY 1000 TGGACATGATGATTTGGCGCTCAAGAGTGCCTGCTCTGCTGCCCAAAAGGA 1059
 |||||||
 Db 54612 TGGACATGATGATTTGGCGCTCAAGAGTGCCTGCTCTGCTGCCCAAAAGGA 54671
 QY 1060 CAGGATCTTCGAGAGATCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1119
 |||||||
 Db 54672 CAGGATCTTCGAGAGATCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 54731
 QY 1120 CTGGACTCCCATTCACATTTACATTCATTAAGCCTTGTTACATCCAGAACTAC 1179
 |||||||
 Db 54732 CTGGACTCCCATTCACATTTACATTCATTAAGCCTTGTTACATCCAGAACTAC 54791
 QY 1180 GTTCCAGACTGTTTCTTGGAGCTTCTGCTATAGTTTACAAACAGCTGCTCAA 1239
 |||||||
 Db 54792 GTTCCAGACTGTTTCTTGGAGCTTCTGCTATAGTTTACAAACAGCTGCTCAA 54851
 QY 1240 CCAGTCTCTTATGATCTGATGAAACTCAACAGATGCTGAGAGTCTGTAT 1299
 |||||||
 Db 54852 CCAGTCTCTTATGATCTGATGAAACTCAACAGATGCTGAGAGTCTGTAT 54911
 QY 1300 CCCAACCTTCTCCACATTTGAGCAGCAACAACTCCACTCGAATTCGTCAGAACTAGAGA 1359
 |||||||
 Db 54912 CCCAACCTTCTCCACATTTGAGCAGCAACAACTCCACTCGAATTCGTCAGAACTAGAGA 54971
 QY 1360 CCACCCCTCCAGGCGCAATACAGTGTAGTAATATATCATCAG 1402
 |||||||
 Db 54972 CCACCCCTCCAGGCGCAATACAGTGTAGTAATATATCATCAG 55014

RESULT 6
 AL136444/c DNA HTG 23-JUL-2000
 LOCUS
 DEFINITION Home sapiens chromosome 6 clone RP3-366F13, *** SEQUENCING IN
 PROGRESS ***
 ACCSSION AL136444
 VERSION
 KEYWORDS AL136444.11 GI:9437221
 SOURCE HTG: HTGS_PHASE1; HTGS_DRAFT.
 ORGANISM human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 131426)
 Direct Submission
 Submitted (22-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 On Jul 24, 2000 this sequence version replaced gi:9368896.
 COMMENT
 Center: Sanger Centre
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquerry@sanger.ac.uk
 Project information
 Center project name: dj366f13
 Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: plasmid; L08752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 130583 bases at least Q40
 Consensus quality: 131107 bases at least Q30
 Consensus quality: 131274 bases at least Q20
 Insert size: 131326; sum-of-ctrls
 Insert size: 140334; 3.3% error; agarose-fp

Quality coverage: 0.00x in Q20 bases; sum-of-ctrls Quality
 coverage: 0.00x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

FEATURES

source

1..131426

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="6"

/clone="RP3-366F13"

/clone_id="RP3-3"

misc.feature

1..130047

misc.feature

130148..131426

BASE COUNT

40768 a 24297 c 24755 g 41506 t 100 others

Query Match

32.5%; Score 523; DB 85; Length 131426;

Best Local Similarity 100.0%; Pred. No. 3e-787;

Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 880 AGGTTCCATAGATTGTACACTATCTCTCATCCCACTGGAGTGGGAAACCTGCT 939
 |||||||
 Db 45747 AGGTTCCATAGATTGTACACTATCTCTCATCCCACTGGAGTGGGAAACCTGCT 45688
 QY 940 GAAGATCTGTGTTTTCATCTTCCCTTCATTAAGCAGTGCATATACCGTGTGCTA 999
 |||||||
 Db 45687 GAAGATCTGTGTTTTCATCTTCCCTTCATTAAGCAGTGCATATACCGTGTGCTA 45628
 QY 1000 TGGACATGATGATTTGGCGCTCAAGAGTGCCTGCTCTGCTGCCCAAAAGGA 1059
 |||||||
 Db 45627 TGGACATGATGATTTGGCGCTCAAGAGTGCCTGCTCTGCTGCCCAAAAGGA 45568
 QY 1060 CAGGATCTTCGAGAGATCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1119
 |||||||
 Db 45567 CAGGATCTTCGAGAGATCCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 45508
 QY 1120 CTGGACTCCCATTCACATTTACATTCATTAAGCCTTGTTACATCCAGAACTAC 1179
 |||||||
 Db 45507 CTGGACTCCCATTCACATTTACATTCATTAAGCCTTGTTACATCCAGAACTAC 45448
 QY 1180 GTTCCAGACTGTTTCTTGGAGCTTCTGCTATAGTTTACAAACAGCTGCTCAA 1239
 |||||||
 Db 45447 GTTCCAGACTGTTTCTTGGAGCTTCTGCTATAGTTTACAAACAGCTGCTCAA 45388
 QY 1240 CCAGTCTCTTATGATCTGATGAAACTCAACAGATGCTGAGAGTCTGTAT 1299
 |||||||
 Db 45387 CCAGTCTCTTATGATCTGATGAAACTCAACAGATGCTGAGAGTCTGTAT 45328
 QY 1300 CCCAACCTTCTCCACATTTGAGCAGCAACAACTCCACTCGAATTCGTCAGAACTAGAGA 1359
 |||||||
 Db 45327 CCCAACCTTCTCCACATTTGAGCAGCAACAACTCCACTCGAATTCGTCAGAACTAGAGA 45268
 QY 1360 CCACCCCTCCAGGCGCAATACAGTGTAGTAATATATCATCAG 1402
 |||||||
 Db 45267 CCACCCCTCCAGGCGCAATACAGTGTAGTAATATATCATCAG 45225

RESULT 7

HSOPRM12 1598 bp DNA PRI 02-DEC-1997
 LOCUS

DEFINITION Homo sapiens mu opioid receptor (OPRM1) gene, partial cds, exons 2 and 3, complete IVS2.

ACCESSION AF024516

VERSION AF024516.1 GI:2655102

KEYWORDS 2 of 3

SEGMENT

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1598)

AUTHORS Wang,J.B., Johnson,P.S., Persico,A.M., Hawkins,A.L., Griffin,C.A. and Uhl,G.R.

TITLE Human mu opiate receptor. cDNA and genomic clones, pharmacologic characterization and chromosomal assignment

JOURNAL FEBS Lett. 338 (2), 217-222 (1994)

MEDLINE 94139928

REFERENCE 2 (bases 1 to 1598)

AUTHORS Bare,L.A., Mansson,E. and Yang,D.

TITLE Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH cells and human brain

JOURNAL FEBS Lett. 354 (2), 213-216 (1994)

MEDLINE 95046336

REFERENCE 3 (bases 1 to 1598)

AUTHORS Bergen,A.W., Kokoszka,J., Peterson,R., Long,J.C., Virkkunen,M., Linnoila,M. and Goldman,D.

TITLE Mu opioid receptor gene variants: lack of association with alcohol dependence

JOURNAL Mol. Psychiatry 2 (6), 490-494 (1997)

MEDLINE 98060615

REFERENCE 4 (bases 1 to 1598)

AUTHORS Bergen,A.W., Kokoszka,J. and Goldman,D.

TITLE Direct Submission

JOURNAL Submitted (11-SEP-1997) Neurogenetics, NIAAA/NIH, 12501 Washington Avenue, Rockville, MD 20852, USA

COMMENT 30 US Caucasian and North American Indian chromosomes were directly sequenced at the OPRM1 locus, exon 2, IVS 2 and exon 3.

FEATURES

source location/qualifiers

1..1598

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="6"

/map="q24-q25"

<1..340

/gene="OPRM1"

/number=2

join(<1..340,1114..>1598)

/gene="OPRM1"

/note="G-protein linked 7 transmembrane protein"

/codon_start=1

/product="mu opioid receptor"

/protein_id="AAC81878.1"

/db_xref="GI:2655106"

/translation="KRTATNIFYFLALADALATSLPQSVNYLMGTWPGTILCKIV ISIDYVMFTSIFLICTMSVDYIAVCHPKALDFPRNAKIIINVCMILSSIGLP VMEMATKYRQSGIDICTLTFESHPTWENLTKICVFEPFARIMPLYLIITVCGMLIARL KSVRMISGSKEDRNLEPRITRMVLYVAVIVCTPTPHIVIIKALVTIETPTQYS WHFCIALGYTNSCNLPVLIAPLDENKRCERFCIPSSNIEQNSRIRONTDHP" 137

/gene="OPRM1"

/note="observed in 1/30 chromosomes corresponding to a S145C (TTC->TGC) substitution"

/replace="g"

319

/gene="OPRM1"

/note="GenBank Accession Number U12569"

/citation=[2]

/replace="a"

341..1113

/gene="OPRM1"

/number=2

1031

/gene="OPRM1"

variation

/note="observed in 12/30 chromosomes"

/replace="g"

1114..>1598

/gene="OPRM1"

/number=3

1169

/gene="OPRM1"

/note="GenBank Accession Number L25119"

/citation=[1]

/replace="c"

1170

/gene="OPRM1"

/note="GenBank Accession Number L25119"

/citation=[1]

/replace="g"

BASE COUNT 477 a 354 c 282 g 485 t

ORIGIN

Query Match 30.2% Score 487; DB 66; Length 1598;

Best Local Similarity 100.0%; Pred. No. 1,1e-266;

Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 880 AGGTTCCATGATGTGACCTAATCATTTCTCATCCAACTGTAAGTAACTGCT 939

|||||

Db 1112 AGGTTCCATGATGTGACCTAATCATTTCTCATCCAACTGTAAGTAACTGCT 1171

QY 940 GAAGATCTGTGTTTCATCTTCCGCTTCATTTATGCGAGTGTCTATACCGTGTGCTA 999

|||||

Db 1172 GAAGATCTGTGTTTCATCTTCCGCTTCATTTATGCGAGTGTCTATACCGTGTGCTA 1231

QY 1000 TGGACTGATGATCTTGGCGCCCAAGAGTGTCCGATGCTCTCTGCTCCAAAGAAAGGA 1059

|||||

Db 1232 TGGACTGATGATCTTGGCGCCCAAGAGTGTCCGATGCTCTCTGCTCCAAAGAAAGGA 1291

QY 1060 CAGGAATCTTGAAGGATACACAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1119

|||||

Db 1292 CAGGAATCTTGAAGGATACACAGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1351

QY 1120 CTGAGCTCCCATTCACATTCATGATCATTAAGCCCTGGTTCAATCCAGAACTAC 1179

|||||

Db 1352 CTGAGCTCCCATTCACATTCATGATCATTAAGCCCTGGTTCAATCCAGAACTAC 1411

QY 1180 GTTCCAGACTGTTCTTGGCACTTCTGATGCTCTAGGTATACAAACAGCTGCTCAA 1239

|||||

Db 1412 GTTCCAGACTGTTCTTGGCACTTCTGATGCTCTAGGTATACAAACAGCTGCTCAA 1471

QY 1240 CCCAGTCTTATGATTCATTTCTGATGAAGAACTTCAACGATGCTTCAGAGTCTGTAT 1299

|||||

Db 1472 CCCAGTCTTATGATTCATTTCTGATGAAGAACTTCAACGATGCTTCAGAGTCTGTAT 1551

QY 1300 CCCAAGCTCTTCACATTCGAGCAACAAACTCCAGTGTGATGCTGAGAACTAGAGA 1359

|||||

Db 1532 CCCAAGCTCTTCACATTCGAGCAACAAACTCCAGTGTGATGCTGAGAACTAGAGA 1577

QY 1360 CCACCCC 1356

|||||

Db 1592 CCACCCC 1598

RESULT 8

AL359850/c

LOCUS Homo sapiens chromosome 6 clone RP11-157M8, *** SEQUENCING IN: PROGRESS ***

ACCESSION AL359850

VERSION AL359850.2 GI:9367619

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 124569)

AUTHORS
TITLE
JOURNAL

COMMENT

Sims, S.
Direct Submission
Submitted (15-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
On Jul 22, 2000 this sequence version replaced g1:8977775.
----- Genome Center

Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: ba157m8

----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 102271 bases at least Q40
Consensus quality: 110329 bases at least Q30
Consensus quality: 115261 bases at least Q20
Insert size: 120669; sum-of-contigs
Quality coverage: 3.24x in Q20 bases; sum-of-contigs quality
coverage: 2.68x in Q20 bases; agarose-tp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 40 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

1 1459: contig of 1459 bp in length
1460 1559: gap of 100 bp
1560 3320: contig of 1761 bp in length
3321 3420: gap of 100 bp
3421 5562: contig of 2142 bp in length
5563 5662: gap of 100 bp
5663 9774: contig of 4112 bp in length
9775 9874: gap of 100 bp
9875 11521: contig of 1647 bp in length
11522 11621: gap of 100 bp
11622 14784: contig of 3163 bp in length
14785 14884: gap of 100 bp
14885 16923: contig of 2045 bp in length
16930 17029: gap of 100 bp
17030 21195: contig of 4166 bp in length
21196 21295: gap of 100 bp
21296 22547: contig of 1252 bp in length
22548 22647: gap of 100 bp
22648 28063: contig of 5416 bp in length
28064 28163: gap of 100 bp
28164 30406: contig of 2243 bp in length
30407 30506: gap of 100 bp
30507 32053: contig of 1547 bp in length
32054 32153: gap of 100 bp
32154 34236: contig of 2083 bp in length
34237 34336: gap of 100 bp
34337 36558: contig of 2222 bp in length
36559 36658: gap of 100 bp
36659 38408: contig of 1750 bp in length
38409 38508: gap of 100 bp
38509 40660: contig of 2152 bp in length
40661 40760: gap of 100 bp
40761 42115: contig of 1355 bp in length
42116 42215: gap of 100 bp
42216 45404: contig of 3189 bp in length
45405 45504: gap of 100 bp
45505 47767: contig of 2263 bp in length
47768 47867: gap of 100 bp
47868 50333: contig of 2466 bp in length
50334 50433: gap of 100 bp

```

FEATURES

SOURCE

```

50434 53910: contig of 3477 bp in length
53911 54010: gap of 100 bp
54011 55124: contig of 1114 bp in length
55125 55224: gap of 100 bp
55225 57215: contig of 1991 bp in length
57216 57315: gap of 100 bp
57316 58382: contig of 1067 bp in length
58383 58482: gap of 100 bp
58483 80755: contig of 22273 bp in length
80756 80855: gap of 100 bp
80856 81866: contig of 1011 bp in length
81867 81966: gap of 100 bp
81967 85210: contig of 3244 bp in length
85211 85310: gap of 100 bp
85311 87074: contig of 1764 bp in length
87075 87174: gap of 100 bp
87175 91511: contig of 4337 bp in length
91512 91611: gap of 100 bp
91612 92650: contig of 1039 bp in length
92651 92750: gap of 100 bp
92751 95618: contig of 2868 bp in length
95619 95718: gap of 100 bp
95719 97538: contig of 1840 bp in length
97539 97638: gap of 100 bp
97639 100174: contig of 2516 bp in length
100175 100274: gap of 100 bp
100275 101789: contig of 1515 bp in length
101790 101889: gap of 100 bp
101890 103053: contig of 1164 bp in length
103054 103153: gap of 100 bp
103154 106517: contig of 3364 bp in length
106518 106617: gap of 100 bp
106618 107662: contig of 1045 bp in length
107663 107762: gap of 100 bp
107763 110688: contig of 2926 bp in length
110689 110788: gap of 100 bp
110789 115340: contig of 4552 bp in length
115341 115440: gap of 100 bp
115441 124569: contig of 9129 bp in length.

location/Qualifiers
1..124569
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RP11-157M8"
/clone_1bp="RP11-11.1"
1..1459
/note="assembly-fragment:01001"
fragment_chain:1
1560..3320
/note="assembly-fragment:00995"
fragment_chain:1
3421..5562
/note="assembly-fragment:00697"
fragment_chain:1
5663..9774
/note="assembly-fragment:01147"
fragment_chain:1
9875..11521
/note="assembly-fragment:00015"
fragment_chain:2
11622..14784
/note="assembly-fragment:01088"
fragment_chain:2
14885..16929
/note="assembly-fragment:01190"
fragment_chain:2
17030..21195
/note="assembly-fragment:00007"
fragment_chain:3
21296..22547
/note="assembly-fragment:00142"
fragment_chain:3

```

```
misc_feature 22648..28063
              /note="assembly_fragment:00116
              fragment_chain:4"
misc_feature 28164..30406
              /note="assembly_fragment:01178
              fragment_chain:4"
misc_feature 30507..32053
              /note="assembly_fragment:00512
              fragment_chain:5"
misc_feature 32154..34236
              /note="assembly_fragment:00924
              fragment_chain:5"
misc_feature 34337..36558
              /note="assembly_fragment:00743
              fragment_chain:6"
misc_feature 36659..38408
              /note="assembly_fragment:00187
              fragment_chain:6"
misc_feature 38509..40660
              /note="assembly_fragment:00749
              fragment_chain:7"
misc_feature 40761..42115
              /note="assembly_fragment:00794
              fragment_chain:7"
misc_feature 42216..45404
              /note="assembly_fragment:01106
              fragment_chain:8"
misc_feature 45505..47767
              /note="assembly_fragment:00346
              fragment_chain:8"
misc_feature 47868..50333
              /note="assembly_fragment:00023"
              fragment_chain:8"
misc_feature 50434..53910
              /note="assembly_fragment:00085"
              fragment_chain:8"
misc_feature 54011..55124
              /note="assembly_fragment:00099"
              fragment_chain:8"
misc_feature 55225..57215
              /note="assembly_fragment:00139"
              fragment_chain:8"
misc_feature 57316..58382
              /note="assembly_fragment:00161"
              fragment_chain:8"
misc_feature 58483..80755
              /note="assembly_fragment:00266"
              fragment_chain:8"
misc_feature 80856..81866
              /note="assembly_fragment:00266"
              fragment_chain:8"

Query Match 25.2% Score 406; DB 88; Length 124569;
Best Local Similarity 99.8%; Pred. No. 2.5e-220;
Matches 526; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 3 GATGAGCCTCTGTGAAGTAAAGTGGAGGGGCTATACGACGAGGAGTATGCAGT 62
    |||||||
Db 39442 GATGAGCCTCTGTGAAGTAAAGTGGAGGGGCTATACGACGAGGAGTATGCAGT 39383
OY 63 GCTCAGCTCGGTCCCTCCGCTGAGGCTCTCTGTCTCAGCCAGGACTGTTCTGT 122
    |||||||
Db 39382 GCTCAGCTCGGTCCCTCCGCTGAGGCTCTCTGTCTCAGCCAGGACTGTTCTGT 39323
OY 123 AAGAAACAGCAGAGACTGTGGCAGGGGGAAGAGAGGCGCTGAGGCGCTTGAACCCGA 182
    |||||||
Db 39322 AAGAAACAGCAGAGACTGTGGCAGGGGGAAGAGAGGCGCTTGAACCCGA 39263
OY 183 AAGAGTCTGGTCTCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
    |||||||
Db 39262 AAGAGTCTGGTCTCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39203
OY 242 GACACAGCGCTGCCGCCAGCAAGCCAGCAATTCACACTGATGCTTGGCTACTCACT 301
    |||||||
Db 39202 GACACAGCGCTGCCGCCAGCAAGCCAGCAATTCACACTGATGCTTGGCTACTCACT 39143
OY 302 TGCTCCCGCAGCAGCCAGCCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
    |||||||
Db 39142 TGCTCCCGCAGCAGCCAGCCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39083
OY 362 TCGCACCATGCGGTCCGAACCGCACGACCTGGCGGGAGAGACAGCTGTGCCCTCCG 421
```

```
Db 39082 TCGCACCATGCGGTCCGAACCGCACGACCTGGCGGGAGAGACAGCTGTGCCCTCCG 39023
|||||
OY 422 ACCGGCACTCCCTCCATGATACAGGCGCATACGATGATGCGCTTACTCCATCTGTGC 481
|||||
Db 39022 ACCGGCACTCCCTCCATGATACAGGCGCATACGATGATGCGCTTACTCCATCTGTGC 38963
|||||
OY 482 GGTGGGGGCTCTTGGAAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 528
|||||
Db 38962 GGTGGGGGCTCTTGGAAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 38915
|||||

RESULT 9
AC027439
LOCUS AC027439 182048 bp DNA HTG 14-JUN-2000
DEFINITION Homo sapiens chromosome 6 clone RP11-30607 map 6, WORKING DRAFT
SEQUENCE, 18 unordered pieces.
ACCESSION AC027439
VERSION AC027439.2 GI:8516101
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 182048)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 6, clone RP11-30607
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 182048)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beta, F.,
Boguslavsky, L., Boukhalter, B., Brown, A., Burrell, G.,
Campopiano, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,
Collins, A., Cooke, P., Dearellano, R., Dewar, K., Diaz, J. S.,
Dodgson, S., Domingo, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardina, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Haefford, A., Horton, L.,
Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Laroque, K., Lamazares, R., Landers, T., Lehotzky, U.,
Levine, R., Lileu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGuck, A., McKernan, K., McPheeters, R.,
Meldrum, J., Menus, L., Mihova, T., Miranda, C., Mlewa, V., Morrow, J.,
Murphy, T., Naylor, T., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Olivier, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tessfay, S., Theodore, J., Turrell, A., Travers, M., Trigglio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 14, 2000 this sequence version replaced gi:7342168.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIPR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center Project name: L8135
Center Clone name: 306_O_7
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 172491 bases at least Q40
Consensus quality: 177577 bases at least Q30
Consensus quality: 179485 bases at least Q20
Insert size: 18800; agarose-fp
```

Insert size: 180348; sum-of-contrigs
Quality coverage: 4.4 in Q20 bases; agarose-ff
Quality coverage: 4.6 in Q20 bases; sum-of-contrigs

NOTE: This is a 'working draft' sequence. It currently
consists of 18 contrigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contrigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 1047: contrig of 1047 bp in length
1048 1147: gap of 100 bp
1148 1354: contrig of 207 bp in length
1355 1454: gap of 100 bp
1455 3155: contrig of 1701 bp in length
3156 3255: gap of 100 bp
3256 6573: contrig of 3318 bp in length
6574 6673: gap of 100 bp
6674 9233: contrig of 2560 bp in length
9234 9333: gap of 100 bp
9334 12513: contrig of 3180 bp in length
12514 12613: gap of 100 bp
12614 18852: contrig of 6239 bp in length
18853 18952: gap of 100 bp
18953 24896: contrig of 5944 bp in length
24897 24996: gap of 100 bp
24997 32904: contrig of 7908 bp in length
32905 33004: gap of 100 bp
33005 41063: contrig of 8059 bp in length
41064 41163: gap of 100 bp
41164 49312: contrig of 8149 bp in length
49313 49412: gap of 100 bp
49413 60412: contrig of 11000 bp in length
60413 60512: gap of 100 bp
60513 73244: contrig of 12732 bp in length
73245 73344: gap of 100 bp
73345 88021: contrig of 14677 bp in length
88022 88121: gap of 100 bp
88122 105702: contrig of 17581 bp in length
105703 105802: gap of 100 bp
105803 131166: contrig of 25364 bp in length
131167 131266: gap of 100 bp
131267 158770: contrig of 27504 bp in length
158771 158870: gap of 100 bp
158871 182048: contrig of 23178 bp in length.

FEATURES

Source
1. 182048
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="6"
/clone="RP11-30607"
/clone_id="RPC1-11 Human Male BAC"
1. 1047
/note="assembly_fragment"
1148. 1354
/note="assembly_fragment"
vector_side:left"
misc_feature
1455. 3155
/note="assembly_fragment"
3256. 6573
/note="assembly_fragment"
6674. 9233
/note="assembly_fragment"
9334. 12513
/note="assembly_fragment"
12614. 18852
/note="assembly_fragment"
18953. 24896
/note="assembly_fragment"

misc_feature 24997..32904
/note="assembly_fragment"
misc_feature 33005..41063
/note="assembly_fragment"
misc_feature 41164..49312
/note="assembly_fragment"
misc_feature 49413..60412
/note="assembly_fragment"
misc_feature 60513..73244
/note="assembly_fragment"
misc_feature 73345..88021
/note="assembly_fragment"
misc_feature 88122..105702
/note="assembly_fragment"
misc_feature 105803..131166
/note="assembly_fragment"
misc_feature 131267..158770
/note="assembly_fragment"
misc_feature 158871..182048
/note="assembly_fragment"
BASE COUNT 55404 a 35093 c 35419 g 54431 t 1701 others
ORIGIN

Query Match 25.2%; Score 406; DB 80; Length 182048;
Best Local Similarity 99.8%; Pred. No. 2.6e-220;
Matches 526; Conservative 0; Mismatches 0; Indels 1; Gaps

3 GATGAGCTCTGTGACACTTAAGTGGGAGGGGCTTACGCAGAGAGAAATGTCAGAT 62
Db 75485 GATGAGCTCTGTGAACTAAGTGGGAGGGGCTTACGCAGAGAGAAATGTCAGAT 75544
OY 63 GCTGAGCTGGTCCCTCGGCTGACGCTCTCTCTCTGTCAGCAGAGAGCTTTCGT 122
Db 75545 GCTGAGCTGGTCCCTCGGCTGACGCTCTCTCTCTGTCAGCAGAGAGCTTTCGT 75604
OY 123 AAGAAACAGCAGAGAGCTGTGACGCGGAGAAAGAGAGCGCTGAGCGCTTGAACCCGA 182
Db 75605 AAGAAACAGCAGAGAGCTGTGACGCGGAGAAAGAGAGCGCTTGAACCCGA 75664
OY 183 AAGTCTGGTGTCTCTGTGCTACTCTGACAGC-GTGGCCCGCGCGGTAGTACCTG 241
Db 75665 AAGTCTGGTGTCTCTGTGCTACTCTGACAGCAGCGTGGCCCGCGGTAGTACCTG 75724
OY 242 GACAGCAGCGTGGCCCGCAGCAAGCGCATTCATGATGCTTGGCTTACTCAAGT 301
Db 75725 GACAGCAGCGTGGCCCGCAGCAAGCGCATTCATGATGCTTGGCTTACTCAAGT 75784
OY 302 TGCTCCCGAGACCCAGCGCGGTCTGTGCTCAACTGTCCCACTTAGATGGCAACCTG 361
Db 75785 TGCTCCCGAGACCCAGCGCGGTCTGTGCTCAACTGTCCCACTTAGATGGCAACCTG 75844
OY 362 TCCGACCATCGGTGTCCGACACCGCACTGGGCGGGGAGAGACAGCTTGCCCTCGG 421
Db 75845 TCCGACCATCGGTGTCCGACACCGCACTGGGCGGGGAGAGACAGCTTGCCCTCGG 75904
OY 422 ACCGCACTCCCTCATGATCAGCGGCATACAGATCATGAGCCCTCTACTCATGCTGTGC 481
Db 75905 ACCGCACTCCCTCATGATCAGCGGCATACAGATCATGAGCCCTCTACTCATGCTGTGC 75964
OY 482 GTGTGGGGCTCTTGGAACCTTCTGTGATGTATGTGATGTCAG 528
Db 75965 GTGTGGGGCTCTTGGAACCTTCTGTGATGTATGTGATGTCAG 76011

RESULT 10
AC021745/c AC021745. 182383 bp DNA HTG 04-APR-2000
LOCUS Homo sapiens chromosome 11 clone RP11-339D1 map 11, WORKING DRAFT
DEFINITION
SEQUENCE 9 unordered pieces.
ACCESSION AC021745.3 GI:7408033
VERSION
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

Db 86129 ACCGACAGTCCCTCCATGATCATGACGACATGATGAGCCCTGACTACATGCTGTGC 86070
 Oy 442 GTGGTGGGCTCTTGGAACTCTCTGTCATGATGATGTCAG 528
 Db 86069 GTGGTGGGCTCTTGGAACTCTCTGTCATGATGATGTCAG 86023

RESULT 11

AC027439/c

LOCUS AC027439 182048 bp DNA HTG 14-JUN-2000
 DEFINITION Homo sapiens chromosome 6 clone RP11-30607 map 6, WORKING DRAFT
 SEQUENCE, 18 unordered pieces.

AC027439

AC027439.2 GI:8516101

HTG: HTGS_PHASE1: HTGS_DRAFT.

KEYWORDS

human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 182048)

2 (bases 1 to 182048)

Unpublished

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

* consists of 18 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1047: contig of 1047 bp in length
 1048 1147: gap of 100 bp
 1148 1354: contig of 207 bp in length
 1355 1454: gap of 100 bp
 1455 3155: contig of 1701 bp in length
 3156 3255: gap of 100 bp
 3256 6573: contig of 3318 bp in length
 6574 6673: gap of 100 bp
 6674 9233: contig of 2560 bp in length
 9234 9333: gap of 100 bp
 9334 12513: contig of 3180 bp in length
 12514 12613: gap of 100 bp
 12614 18852: contig of 6239 bp in length
 18853 18952: gap of 100 bp
 18953 24896: contig of 5944 bp in length
 24897 24996: gap of 100 bp
 24997 32904: contig of 7908 bp in length
 32905 33004: gap of 100 bp
 33005 41063: contig of 8059 bp in length
 41064 41163: gap of 100 bp
 41164 49312: contig of 8149 bp in length
 49313 49412: gap of 100 bp
 49413 60412: contig of 11000 bp in length
 60413 60512: gap of 100 bp
 60513 73244: contig of 12732 bp in length
 73245 73344: gap of 100 bp
 73345 88021: contig of 14677 bp in length
 88022 88121: gap of 100 bp
 88122 105702: contig of 17351 bp in length
 105703 105802: gap of 100 bp
 105803 131166: contig of 25364 bp in length
 131167 131266: gap of 100 bp
 131267 158770: contig of 27504 bp in length
 158771 158870: gap of 100 bp
 158871 182048: contig of 23178 bp in length.

FEATURES

source

1. 182048
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6"
 /clone="RP11-30607"
 /clone_1b="RPC1-11 Human Male BAC"
 1. 1047
 /note="assembly_fragment"
 1148. 1354
 /note="assembly_fragment"
 clone_end:SP6
 vector_side:left
 1455. 3155
 /note="assembly_fragment"
 3256. 6573
 /note="assembly_fragment"
 6674. 9233
 /note="assembly_fragment"
 9334. 12513
 /note="assembly_fragment"
 12614. 18852
 /note="assembly_fragment"
 18953. 24896
 /note="assembly_fragment"
 24997. 32904
 /note="assembly_fragment"
 33005. 41063
 /note="assembly_fragment"
 41164. 49312
 /note="assembly_fragment"

* NOTE: This is a 'working draft' sequence. It currently

misc_feature /note="assembly_fragment"
49413..60412
misc_feature /note="assembly_fragment"
60513..73244
misc_feature /note="assembly_fragment"
73345..88021
misc_feature /note="assembly_fragment"
88122..105702
misc_feature /note="assembly_fragment"
105803..131166
misc_feature /note="assembly_fragment"
131267..158770
misc_feature /note="assembly_fragment"
158871..182048
BASE COUNT 55404 a 35093 c 35419 g 54431 t 1701 others
ORIGIN

Query Match 22.2%; Score 357; DB 80; Length 182048;
Best Local Similarity 100.0%; Pred. No. 2.7e-192;
Matches 357; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 527 AGATACACCAAGATGAGACTGCGACCAACATCTACATTTTCAACCTTGCTGGCAGAT 586
|||||
DB 7997 AGATACACCAAGATGAGACTGCGACCAACATCTACATTTTCAACCTTGCTGGCAGAT 7938
QY 587 GCCTTACCAACAGTACCTGCGCTCCAGAGTGTGAATTAATCTTAATGGAAATGSCCA 646
|||||
DB 7937 GCCTTACCAACAGTACCTGCGCTCCAGAGTGTGAATTAATCTTAATGGAAATGSCCA 7878
QY 647 TTGGAAACCATCTTTCAGATAGTATGATCCCATATTAATTAATGTTTACCAGC 706
|||||
DB 7877 TTGGAAACCATCTTTCAGATAGTATGATCCCATATTAATTAATGTTTACCAGC 7818
QY 707 ATATTCACCTTCGACCATGAGTGTGATGATACATTGAGAGTGTGCCACCTGTCAAG 766
|||||
DB 7817 ATATTCACCTTCGACCATGAGTGTGATGATACATTGAGAGTGTGCCACCTGTCAAG 7758
QY 767 GCCTTACATTCGCTACTCCCGCAATGCAAAATATCAATGCTGTCCAACTGGATCTC 826
|||||
DB 7757 GCCTTACATTCGCTACTCCCGCAATGCAAAATATCAATGCTGTCCAACTGGATCTC 7698
QY 827 TCTTACACCATGCTGCTCTCTGATGATGCTCATGCTCAACAAATACAGGCAAGT 883
|||||
DB 7697 TCTTACACCATGCTGCTCTCTGATGATGCTCATGCTCAACAAATACAGGCAAGT 7641

RESULT 12
AF286024 1203 bp mRNA PRI 03-ANG-2000
LOCUS Macaca mulatta mu opioid receptor mRNA, complete cds.
DEFINITION AF286024
ACCESSION AF286024.1 GI:9664878
VERSION
KEYWORDS
SOURCE
ORGANISM
rhesus monkey.
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
1 (bases 1 to 1203)
Muller, G.M. and Madras, B.K.
Cloning of the Macaca mulatta mu opioid receptor
Unpublished
2 (bases 1 to 1203)
REFERENCE
AUTHORS Miller, G.M. and Madras, B.K.
TITLE Direct Submission
JOURNAL Submitted (11-JUL-2000) Neurochemistry, New England Regional
Primate Research Center, Harvard Medical School, One Pine Hill
Drive, Southborough, MA 01772, USA
Location/Qualifiers
1..1203
/organism="Macaca mulatta"

CDS
/db_xref="taxon:9544"
/tisue_type="striatum"
1..1203
/codon_start=1
/product="mu opioid receptor"
/protein_id="AAF97249.1"
/db_xref="GI:9664878"

BASE COUNT 299 a 350 c 242 g 312 t
ORIGIN

Query Match 16.6%; Score 267; DB 11; Length 1203;
Best Local Similarity 99.0%; Pred. No. 7.7e-141;
Matches 567; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 316 CAGCCCGGTTCTCGGATCACTTGCCCACTAGATGGCAACCTGCGACCCATGCGG 375
|||||
DB 78 CAGCCCGGTTCTCGGATCACTTGCCCACTAGATGGCAACCTGCGACCCATGCGG 137
QY 376 TCGGAACCGACGACCTGGGCGGAGAGACAGCTGTGCTCGACCGGAGTCCCTC 435
|||||
DB 138 TCGGAACCGACGACCTGGGCGGAGAGACAGCTGTGCTCGACCGGAGTCCCTC 157
QY 436 CAGATACGCGCCATACAGTATGAGCCCTCTACTCATGTGTGGTGGGCTCTT 495
|||||
DB 198 CAGATACGCGCCATACAGTATGAGCCCTCTACTCATGTGTGGTGGGCTCTT 257
QY 496 CGGAACCTCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 555
|||||
DB 258 CGGAACCTCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 317
QY 556 CATCTACATTTTCAACCTGCTGTGGAGATGCTTAGCCACGAGTACCTGCTTCCA 615
|||||
DB 318 CATCTACATTTTCAACCTGCTGTGGAGATGCTTAGCCACGAGTACCTGCTTCCA 377
QY 616 GAGTGTGAATTAATGAGGACATGCGCATTTGGACCATCTTTGCAAGTATGAT 675
|||||
DB 378 GAGTGTGAATTAATGAGGACATGCGCATTTGGACCATCTTTGCAAGTATGAT 437
QY 676 CTCATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 735
|||||
DB 438 CTCATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 497
QY 736 TCGATACATTCAGTGTGCGACCCCTGCAAGGCTTAGATTTCCGATCCCGGAATGC 795
|||||
DB 498 TCGATACATTCAGTGTGCGACCCCTGCAAGGCTTAGATTTCCGATCCCGGAATGC 557
QY 796 CAAATATATCAATGCTGCAATGATGATGATGATGATGATGATGATGATGATGAT 855
|||||
DB 558 CAAATATATCAATGCTGCAATGATGATGATGATGATGATGATGATGATGATGAT 617
QY 856 CATGCTACAAACAAATACAGGCAAGTTCAT 888
|||||
DB 618 CATGCTACAAACAAATACAGGCAAGTTCAT 650

RESULT 13
HSOPRM11
LOCUS HSOPRM11 305 bp DNA PRI 02-DEC-1997
DEFINITION Homo sapiens mu opioid receptor (OPRM1) gene, partial cds, exon 1.
ACCESSION AF024515
VERSION AF024515.1 GI:2655101
KEYWORDS
SEGMENT 1 of 3
SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 305)
 Wang, J.B., Johnson, P.S., Persico, A.M., Hawkins, A.L., Griffin, C.A.
 and Uhl, G.R.
 Human mu opiate receptor. cDNA and genomic clones, pharmacologic
 characterization and chromosomal assignment
 FEBS Lett. 338 (2), 217-222 (1994)

JOURNAL
 MEDLINE 94139928
 TITLE 2 (bases 1 to 305)
 AUTHOR Bares, L.A., Mansson, E. and Yang, D.
 TITLE Expression of two variants of the human mu opiate receptor mRNA in
 SK-N-SH cells and human brain
 FEBS Lett. 354 (2), 213-216 (1994)

JOURNAL
 MEDLINE 95046336
 TITLE 3 (bases 1 to 305)
 AUTHOR Bergen, A.W., Kokoszka, J., Peterson, R., Long, J.C., Virkkunen, M.,
 Linnoila, M. and Goldman, D.
 TITLE Mu opiate receptor gene variants: lack of association with alcohol
 dependence
 Mol. Psychiatry 2 (6), 490-494 (1997)

JOURNAL
 MEDLINE 98060615
 TITLE 4 (bases 1 to 305)
 AUTHOR Bergen, A.W., Kokoszka, J. and Goldman, D.
 TITLE Direct Submission
 Submitted (11-SEP-1997) Neurogenetics, NIAAA/NIH, 12501 Washington
 Avenue, Rockville, MD 20852, USA

COMMENT 134 US Caucasian and North American Indian chromosomes were
 directly sequenced at the OPRM1 locus, 5' UTR and Exon 1.
 Location/Qualifiers
 1..305

FEATURES
 source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6q24-q25"
 <1..37
 /gene="OPRM1"
 <1..>305
 /gene="OPRM1"
 /number=1
 38..>305
 /gene="OPRM1"
 /note="G-protein linked 7 transmembrane protein"
 /codon_start=1
 /product="mu opiate receptor"
 /protein_id="AAC51877.1"
 /db_xref="GI:265105"
 /translation="MDSAXPTNASNCTDALAYSSGSPAPSGSVNLSHLDGNLSDP
 CGPNRTDLGGRDLSLCPPTSPMTAITIMALYSIVCVGLFGNF"
 137
 /gene="OPRM1"
 /note="results in a A6V (GCC->GTC) substitution, observed
 in 2/134 chromosomes"
 /replace="c"
 155
 /gene="OPRM1"
 /note="results in a N40D (AAC->GAC) substitution observed
 in 63/134 chromosomes. Asn40 is a phylogenetically
 conserved asparagine in the sequence motif required for
 N-glycosylation. This substitution observed in the cDNA
 sequence of Genbank Accession Number U12569 [Bares et al.,
 1994]"
 /replace="g"
 188
 /gene="OPRM1"
 /note="Genbank Accession Number L25119"
 /citation=[1]
 /replace="a"
 220
 /gene="OPRM1"
 /note="Genbank Accession Number U12569"
 /citation=[2]

variation
 /note="results in a A6V (GCC->GTC) substitution, observed
 in 2/134 chromosomes"
 /replace="c"
 155
 /gene="OPRM1"
 /note="results in a N40D (AAC->GAC) substitution observed
 in 63/134 chromosomes. Asn40 is a phylogenetically
 conserved asparagine in the sequence motif required for
 N-glycosylation. This substitution observed in the cDNA
 sequence of Genbank Accession Number U12569 [Bares et al.,
 1994]"
 /replace="g"
 188
 /gene="OPRM1"
 /note="Genbank Accession Number L25119"
 /citation=[1]
 /replace="a"
 220
 /gene="OPRM1"
 /note="Genbank Accession Number U12569"
 /citation=[2]

conflict
 /note="Genbank Accession Number U12569"
 /citation=[2]

BASE COUNT 54 a 115 c 79 g 56 t 1 others
 ORIGIN
 Query Match 15.6%; Score 251; DB 66; Length 305;
 Best local Similarity 100.0%; Pred. No. 1,1e-131;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 CCCACGAGACGCGACGATTTGACATGCTTGCGGTACTCAAGTTGCTCCACACG 315
 |||
 Db 55 CCCACGAGACGCGACGATTTGACATGCTTGCGGTACTCAAGTTGCTCCACACG 114
 |||

QY 316 CAGCCCGGTTCTGGGTGAACCTTGCCACTAGATGCAACCTTCCGACCATGCGG 375
 |||
 Db 115 CAGCCCGGTTCTGGGTGAACCTTGCCACTAGATGCAACCTTCCGACCATGCGG 174
 |||

QY 376 TCGAACCGCAGACCTGCGGCGGAGACAGACCTGTCCTCCGACCGGAGTCCCTC 435
 |||
 Db 175 TCGAACCGCAGACCTGCGGCGGAGAGACAGACCTGTCCTCCGACCGGAGTCCCTC 234
 |||

QY 436 CATGATCAGGCGCATCATGATGACCTTACTCATCGTGTGCTGGGCTCTT 495
 |||
 Db 235 CATGATCAGGCGCATCATGATGACCTTACTCATCGTGTGCTGGGCTCTT 294
 |||

QY 496 CGGAACCTTC 506
 |||
 Db 295 CGGAACCTTC 305
 |||

RESULT 14
 AF153500 AF153500 3759 bp DNA PRI 18-JUL-1999
 LOCUS Homo sapiens mu opiate receptor (MOR1) gene, partial cds.
 DEFINITION AF153500
 ACCESSION AF153500
 VERSION AF153500.1 GI:5524612
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 3759)
 Uhl, G.R., Sora, I. and Wang, Z.
 The mu opiate receptor as a candidate gene for pain: Polymorphisms,
 variations in expression, nociception, and opiate responses
 Proc. Natl. Acad. Sci. U.S.A. 96 (14), 7752-7755 (1999)

JOURNAL
 MEDLINE 94139928
 TITLE 2 (bases 1 to 3759)
 AUTHOR Wang, Z., Sora, I. and Uhl, G.R.
 TITLE Direct Submission
 Submitted (23-MAY-1999) Molecular Neurobiology, NIH/NIDA/IRP, P.O.
 Box 5180, Baltimore, MD 21224, USA

JOURNAL
 MEDLINE 95046336
 TITLE 3 (bases 1 to 3759)
 AUTHOR Bergen, A.W., Kokoszka, J., Peterson, R., Long, J.C., Virkkunen, M.,
 Linnoila, M. and Goldman, D.
 TITLE Mu opiate receptor gene variants: lack of association with alcohol
 dependence
 Mol. Psychiatry 2 (6), 490-494 (1997)

FEATURES
 source
 1..3759
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 <3620..>3759
 /gene="MOR1"
 /product="mu opiate receptor"
 <3620..>3759
 /gene="MOR1"
 3620..>3759
 /gene="MOR1"
 /note="G-protein coupled receptor"
 /codon_start=1
 /product="mu opiate receptor"
 /protein_id="AAD44318.1"
 /db_xref="GI:5524613"
 /translation="MDSAXPTNASNCTDALAYSSGSPAPSGSVNLSHLDGNLSDP
 CGP"

BASE COUNT 1237 a 691 c 712 g 1119 t
 ORIGIN

Query Match 13.4% Score 215; DB 11; Length 3759;
 Best Local Similarity 99.7%; Pred. No. 4.3e-111;
 Matches 335; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

OY 44 GCACAGGAGATGTCAGATGCTGAGTGGTCCCTCCGCTGAGAGCTCTGTCTC 103
    |||||||
Db 3424 GCACAGGAGATGTCAGATGCTGAGTGGTCCCTCCGCTGAGAGCTCTGTCTC 3483
OY 104 AGCCAGAGACTGGTTCTGTAAAGAAACAGCAGAGCTGTGGACGGCGAAAGAGCGGC 163
    |||||||
Db 3484 AGCCAGAGACTGGTTCTGTAAAGAAACAGCAGAGCTGTGGACGGCGAAAGAGCGGC 3543
OY 164 TGAGGCGGTTGGAAACCGGAAAGTCTGGTCTCTGCTACCTCGCAGACG-GTGGCGG 222
    |||||||
Db 3544 TGAGGCGGTTGGAAACCGGAAAGTCTGGTCTCTGCTACCTCGCAGACGAGGCGGCGG 3603
OY 223 CCCGGCGCTCAGTACATGACAGCAGCGCTGCCCGCCAGAGCGCAGCAATTGCACTGA 282
    |||||||
Db 3604 CCCGGCGCTCAGTACATGACAGCAGCGCTGCCCGCCAGAGCGCAGCAATTGCACTGA 3663
OY 283 TGCTTGGCTGACTCAAGTCTCTCCAGACACCGCCGGTCTGTGCTCACTGTCTC 342
    |||||||
Db 3664 TGCTTGGCTGACTCAAGTCTCTCCAGACACCGCCGGTCTGTGCTCACTGTCTC 3723
OY 343 CCACCTATGATGCAACCTGTCCGACCCCATGGGCTCC 378
    |||||||
Db 3724 CCACCTATGATGCAACCTGTCCGACCCCATGGGCTCC 3759
  
```

```

RESULT 15
HSDJ402L9 PRI 03-MAR-2000
LOCUS HSDJ402L9 98104 bp DNA
DEFINITION Human DNA sequence from clone RP3-402L9 on chromosome 6q25-26.1.
            Contains the 3' end of the gene for mu opiate receptor (MOR1), the
            3' end of the gene KIAA0403, ESTs, STSs and GSSs, complete
            sequence.
ACCESSION AL132774
VERSION AL132774.20 GI:6706887
KEYWORDS HTG; KIAA0403; MOR1; opiate receptor.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 98104)
AUTHORS Phillimore, B.
JOURNAL Direct Submission
            Submitted (14-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
            Requests: clonerequest@sanger.ac.uk
COMMENT On Jan 16, 2000 this sequence version replaced gi:6691954.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence has been finished according to sequence map criteria
            as follows. An attempt is made to resolve all sequencing problems,
            such as compressions and repeats, but not necessarily within known
            annotated human repeat sequence elements (e.g. Alu). Where the
            sequence is ambiguous, there is an annotation using the 'unsure'
            feature key.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep
            From the library RPCI-3 constructed at the Roswell Park Cancer
            Institute by the group of Pieter de Jong. For further details see
            http://bacpac.med.buffalo.edu/
            VECTOR: pCYPAC2
            This sequence is the entire insert of clone RP3-402L9 This sequence
  
```

FEATURES

was generated from part of bacterial clone contigs of human
 chromosome 6, constructed by the Sanger Centre Chromosome 5 Map
 Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Ch6>.
 Location/Qualifiers

```

source
1..98104
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="q25-26.1"
/clone="RP3-402L9"
/clone_1lb="RPCI-3"
199..573
misc_feature
/note="match: GSS: Em:AQ085222"
709..1171
repeat_region
/note="MER41A repeat: matches 1..467 of consensus"
1188..3645
repeat_region
/note="MER41-internal repeat: matches 1415..3944 of
consensus"
2966..4247
repeat_region
/note="MER51-internal repeat: matches 3576..4921 of
consensus"
3866..4332
repeat_region
/note="MER57-internal repeat: matches 3355..3834 of
consensus"
4329..4383
repeat_region
/note="MER57-internal repeat: matches 2777..2834 of
consensus"
4380..4455
repeat_region
/note="MER57-internal repeat: matches 2549..2626 of
consensus"
4383..4511
repeat_region
/note="HDBRS-P3b repeat: matches 3150..3283 of consensus"
4511..5898
repeat_region
/note="MER57-internal repeat: matches 305..720 of
consensus"
6493..6567
repeat_region
/note="LIMA10 repeat: matches 6246..6319 of consensus"
6932..6971
repeat_region
/note="20 copies 2 mer tg 100% conserved"
7746..8055
repeat_region
/note="AluY repeat: matches 1..311 of consensus"
8280..8683
misc_feature
/note="match: GSS: Em:AQ45108"
8896..9203
repeat_region
/note="AluYb8 repeat: matches 1..316 of consensus"
9384..9675
repeat_region
/note="LTR40b repeat: matches 151..460 of consensus"
9878..10129
repeat_region
/note="HERV40 repeat: matches 5247..5505 of consensus"
10234..10306
repeat_region
/note="HERV40 repeat: matches 5175..5252 of consensus"
10611..11070
repeat_region
/note="HERV40 repeat: matches 4582..5031 of consensus"
11083..11147
repeat_region
/note="HERV40 repeat: matches 2597..2660 of consensus"
11596..12264
repeat_region
/note="HERV40 repeat: matches 1431..2113 of consensus"
12402..12690
repeat_region
/note="AluYb repeat: matches 6..294 of consensus"
12414..12871
misc_feature
/note="match: GSS: Em:AQ040924"
13448..13753
repeat_region
/note="AluX repeat: matches 5..312 of consensus"
14486..14736
repeat_region
/note="LTR40a repeat: matches 151..480 of consensus"
14998..15027
repeat_region
/note="15 copies 2 mer gt 100% conserved"
15818..16598
misc_feature
/note="match: STS: Em:U25119"
<15822..16936
misc_feature
/note="match: cDNAs: Em:U35424 Em:U89677 Em:U19380
/gene="d402L9.1"
  
```



```

Em:D16349 Em:L38645 Em:L29301 Em:L20684 Em:U26915
Em:L25119 Em:L13069"
/notice="not experimental"
/product="d440219.1 (mu opiate receptor (MOR1))"
15822..16936
/gene="d440219.1"
<15822..15860
/gene="d440219.1"
/codon.start=1
/evidence="not experimental"
/product="d440219.1 (mu opiate receptor (MOR1))"
/db.xref="GI:7161755"
/translation="LENIKAEAPLP"
15861..16260
/gene="d440219.1"
/notice="match: STS: Em:G11298"
16869..16874
/gene="d440219.1"
complement(19456..20016)
/notice="match: GSS: Em:AQ373438"
19965..20256
/notice="MER61E repeat: matches 341..635 of consensus"
20365..20430
/notice="MER61E repeat: matches 99..160 of consensus"
20442..20518
/notice="LTR25 repeat: matches 255..333 of consensus"
20658..21195
/notice="MER41B repeat: matches 1..542 of consensus"
complement(21441..21938)
/notice="match: GSS: Em:B70321"
22930..23240
/notice="AluYa5 repeat: matches 1..311 of consensus"
23970..24259
/notice="AluYa9 repeat: matches 2..294 of consensus"
26151..26633
/notice="LTR2 repeat: matches 3..449 of consensus"
26970..27025
/notice="28 copies 2 mer ca 82% conserved"
27305..27606
/notice="AluY repeat: matches 1..304 of consensus"
27794..27923
/notice="65 copies 2 mer ta 58% conserved"
29979..30286
/notice="AluY repeat: matches 1..308 of consensus"
30392..30527
/notice="L2 repeat: matches 2114..2248 of consensus"
30530..30665
/notice="LIM4 repeat: matches 5679..5792 of consensus"
30772..31062
/notice="LIM4 repeat: matches 4591..4911 of consensus"
31187..31284
/notice="L2 repeat: matches 2132..2229 of consensus"
complement(31359..31786)
/notice="match: GSS: Em:AQ170692"
complement(31732..32230)
/notice="match: GSS: Em:AQ600634"
complement(31826..32245)
/notice="match: GSS: Em:AQ440598"
31830..32209
/notice="match: GSS: Em:AQ039738"
32280..32753
/notice="match: GSS: Em:AQ433448"
32326..32616
/notice="AluX repeat: matches 1..290 of consensus"
32617..32678
/notice="31 copies 2 mer ta 83% conserved"
34097..34271
/notice="MIR repeat: matches 75..262 of consensus"
complement(34529..35091)
/notice="match: GSS: Em:AQ896445"
35219..35380
/notice="MIR repeat: matches 11..212 of consensus"

repeat_region 35487..35622
/notice="MER5B repeat: matches 30..157 of consensus"
repeat_region 35698..36377
/notice="LTR8 repeat: matches 1..691 of consensus"
repeat_region 37467..37768
/notice="AluX repeat: matches 1..303 of consensus"
repeat_region 38174..38210
/notice="tRNA-Glu-GAG repeat: matches 1..37 of consensus"
repeat_region 38608..39053
/notice="MER42 repeat: matches 1..504 of consensus"
repeat_region 39278..39978
/notice="MER50 repeat: matches 1..734 of consensus"
repeat_region 40338..40512

Query Match 13.0%; Score 209; DB 66; Length 98104;
Best Local Similarity 100.0%; Pred. No. 1.2e-107;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1399 TCACCTAGAAATCTGAGACAGAAACTGCTCCGTTCCCTAACAGGGTCCATGCATT 1458
|||||
Db 15818 TCACCTAGAAATCTGAGACAGAAACTGCTCCGTTCCCTAACAGGGTCCATGCATT 15877
|||||
QY 1459 CCGACCTTCACCAAGCTTAGAGCCACCATGATGTGGAAGCAGTTGCTTCAAGATGT 1518
|||||
Db 15878 CCGACCTTCACCAAGCTTAGAGCCACCATGATGTGGAAGCAGTTGCTTCAAGATGT 15937
|||||
QY 1519 GTAGAGGCTCTATTCTCAGAAAGTGCCTTTAGCTATCCACCTCTTCTC 1578
|||||
Db 15938 GTAGAGGCTCTATTCTCAGAAAGTGCCTTTAGCTATCCACCTCTTCTC 15997
|||||
QY 1579 TCTGGCCACTCTGCTCTGCACATTAGAGG 1607
|||||
Db 15998 TCTGGCCACTCTGCTCTGCACATTAGAGG 16026
|||||

RESULT 16
G53082 520 bp DNA STS 30-MAR-2000
LOCUS SHGC-84785 Human Homo sapiens STS genomic, sequence tagged site.
DEFINITION G53082
ACCESSION G53082.1 GI:5224409
VERSION
KEYWORDS STS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 520)
AUTHORS Olivier,M. and Cox,D.R.
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL Unpublished (2000)
COMMENT

Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: oliviereshg@stanford.edu
Primer A: TTACCTCCCTCTTCACTCTC
Primer B: ACTGTCCCACTTAGATGCGAAC
STS size: 307
PCR Profile:
Initial incubation: 95 degrees C for 10 minutes
Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 30 seconds
Polymerization: 72 degrees C for 23 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9700

Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Amplifrag Gold Polymerase: 0.07 units/ul

```

Total Vol: 5 u1

Buffer:

MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3

BAC ends sequenced at TIGR from the Rpl11 BAC library. Designed and developed at the Stanford Human Genome Center.

FEATURES

Location/Qualifiers

1..520

/organism="Homo sapiens"

/db_xref="taxon:9606"

/map="6"

/clone_lib="Human"

STS

primer_bind

complement(351..373)

101 a 154 c 153 g 112 t

BASE COUNT

ORIGIN

Query Match 12.9%; Score 207; DB 91; Length 520;

Best Local Similarity 100.0%; Pred. No. 1.6e-106;

Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

322 CGTTCTGGGTCAACTTGTCCCACTAGATGCGCACTGTCCGACCATCGGTCCGAA 381

387 CGGTCTGGGTCAACTTGTCCCACTAGATGCGCACTGTCCGACCATCGGTCCGAA 328

382 CGGACCGACCTGGGCGGAGAGAGACAGCCTGTCCGACCGGACATCCCTCATGAT 441

327 CGGACCGACCTGGGCGGAGAGAGACAGCCTGTCCGACCGGACATCCCTCATGAT 268

442 CACGCGCATCAGATCATGAGCCCTCTACTCCATGCTGTGCGGCTCTTCGAAA 501

267 CACGCGCATCAGATCATGAGCCCTCTACTCCATGCTGTGCGGCTCTTCGAAA 208

502 CTTCCTGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528

207 CTTCCTGTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 181

RESULT 17

AF100548

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

JOURNAL

TITLE

AUTHORS

JOURNAL

MEDLINE

JOURNAL

TITLE

AUTHORS

JOURNAL

MEDLINE

JOURNAL

TITLE

AUTHORS

JOURNAL

CDS

<1..>293

/codon_start=1

/product="mu-opioid receptor"

/protein_id="AF04722.1"

/db_xref="GI:6165841"

/translation="LRRITRMVLYVAVAVICWTPPIHIVYILALVITPETPOTVSW
HFCIALGYTMSCLPVLVAFVLDENFRFCRFECIPRISVIEQNSRIRHONTR"

BASE COUNT

ORIGIN

75 a 79 c 56 g 83 t

Query Match

Best Local Similarity 100.0%; Pred. No. 8.9e-69;

Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1172 GAACACGCTCCGACCTGTTCTTGGACATCTGCACTGCTAGTACACAAACAGC 1231

106 GAACTACGCTCCGACCTGTTCTTGGACATCTGCACTGCTAGTACACAAACAGC 165

1232 TGCCTCAACCCAGCTCTTATGCACTTCTGATGAAACCTCAACGATGCTCAGAG 1291

166 TGCCTCAACCCAGCTCTTATGCACTTCTGATGAAACCTCAACGATGCTCAGAG 225

1292 TTCTGTATCCCAACCTCTCC 1312

226 TTCTGTATCCCAACCTCTCC 246

RESULT 18

G11298

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

Unpublished (1995)

Contact: Richard M. Myers

Stanford Human Genome Center (SHGC)

Stanford University School of Medicine

Department of Genetics, M-344, Stanford, CA 94305, USA

Tel: 415/7259687

Fax: 415/7259689

Email: myers@shgc.stanford.edu

Primer A: CATGCCATTCGACCTTC

Primer B: AGGCATTTCTAGAGAAATTAGAGC

STS size: 101

PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng

Primer: each 1 uM

dNTPs: each 200 uM

Tag Polymerase: 0.05 units/u1

Total Vol: 10 u1

Buffer:

MgCl2: 2.5 mM

KCl: 50 mM

Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs derived from U25119 -- Unigene
location/Qualifiers

```
STS          9. .109
primer_bind  9. .26
primer_bind  complement(85. .109)
BASE COUNT  122 a      89 c      83 g      106 t
ORIGIN
```

Query Match	7.1%	Score 115;	DB 91;	length 400;
Best Local Similarity	99.4%	Pred. No. 6.7e-54;		
Matches 165;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Dy 1502 GGTTGCTTCAAGAAATGTGTAGGAGCGCTTAATTCTCTAGGAAGAAGTGCCGCTTTTAGGC 1566
|||||
Dd 61 GGTTCCTTCAAGAAATGTGTAGGAGCGCTTAATTCTCTAGGAAGAAGTGCCCTTTTAGGC 120

Qy 1562 ATCCAACTCTTTCTCTCTGCGCACTCTGCTGCACATTAGAGG 1607
 |||||
 Db 121 ATCCAACTCTTTCTCTCTGCGCACTCTGCTGCACATTAGAGG 166

RESULT	19				
LOCUS	G13328				
DEFINITION	G13328	human SRS UTR-9720.	DNA	SRS	20-DEC-1995
ACCESSION	G13328				
VERSION	G13328.1	GI:1127337			
KEYWORDS		SRS sequence; primer; sequence tagged site.			
SOURCE		human SRS derived from miscellaneous published sequences.			
ORGANISM		Homo sapiens			

FEATURES	COMMENT
source	Avenue, Rockville, MD 20852, USA
	30 US Caucasian and North American Indian chromosomes were directly sequenced at the OPRM1 locus, 3'UTR.
	Location/Qualifiers
	1. .669

JOURNAL
REFERENCE
AUTHORSTITLE
JOURNAL
COMMENT

Unpublished
2 (bases 1 to 77313)
Barren, B., Linton, L., Nushbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckert, R., Bida, F.,
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Castle, A.,
Choepe, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeRellano, K., Dewar, K., Domino, M., Doyle, M., Fennestor, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Gargan, J.,
Gardina, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howard, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lander, E., Lehoczy, J., Levine, R., Lien, C., Liu, G., Locke, K.,
McDonald, P., Marquis, N., McEwan, P., McCurt, A., McKernan, K.,
McNeesters, R., Meldrum, J., Menus, L., Morrow, J., Naylor, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, T. M., Peterson, K.,
Pierre, N., Pisanic, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Tirelli, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
Zimmer, A. and Zody, M.
Direct Submission
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced g1:6922183.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: W1BR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L6177
Center clone name: 310_M_4
* NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
876 975: contig of 875 bp in length
976 1889: contig of 914 bp in length
1890 1989: gap of 100 bp
1990 2894: contig of 905 bp in length
2895 2994: gap of 100 bp
2995 3861: contig of 867 bp in length
3862 3961: gap of 100 bp
3962 4832: contig of 871 bp in length
4833 4932: gap of 100 bp
4933 5840: contig of 908 bp in length
5841 5940: gap of 100 bp
5941 6823: contig of 883 bp in length
6824 6923: gap of 100 bp
6924 7830: contig of 907 bp in length
7831 7930: gap of 100 bp
7931 8844: contig of 914 bp in length
8845 8944: gap of 100 bp
8945 9870: contig of 926 bp in length
9871 9970: gap of 100 bp
9971 10835: contig of 865 bp in length
10836 10935: gap of 100 bp
10936 11840: contig of 905 bp in length
11841 11940: gap of 100 bp
11941 12816: contig of 876 bp in length
12817 12916: gap of 100 bp
12917 13799: contig of 883 bp in length

13800 13899: gap of 100 bp
13900 14784: contig of 885 bp in length
14785 14884: gap of 100 bp
14885 15776: contig of 892 bp in length
15777 15876: gap of 100 bp
15877 16773: contig of 897 bp in length
16774 16873: gap of 100 bp
16874 17772: contig of 899 bp in length
17773 17872: gap of 100 bp
17873 18790: contig of 918 bp in length
18791 18890: gap of 100 bp
18891 19745: contig of 855 bp in length
19746 19845: gap of 100 bp
19846 20749: contig of 904 bp in length
20750 20849: gap of 100 bp
20850 21718: contig of 869 bp in length
21719 21818: gap of 100 bp
21819 22692: contig of 874 bp in length
22693 22792: gap of 100 bp
22793 23653: contig of 861 bp in length
23654 23753: gap of 100 bp
23754 24628: contig of 876 bp in length
24630 24729: gap of 100 bp
24730 25603: contig of 874 bp in length
25604 25703: gap of 100 bp
25704 26550: contig of 847 bp in length
26551 26650: gap of 100 bp
26651 27562: contig of 912 bp in length
27563 27662: gap of 100 bp
27663 28573: contig of 911 bp in length
28574 28673: gap of 100 bp
28674 29587: contig of 914 bp in length
29588 29687: gap of 100 bp
29688 30564: contig of 877 bp in length
30565 30664: gap of 100 bp
30665 31568: contig of 904 bp in length
31569 31668: gap of 100 bp
31669 32538: contig of 870 bp in length
32539 32638: gap of 100 bp
32639 33543: contig of 905 bp in length
33544 33643: gap of 100 bp
33644 34549: contig of 906 bp in length
34550 34649: gap of 100 bp
34650 35551: contig of 902 bp in length
35552 35651: gap of 100 bp
35652 36514: contig of 863 bp in length
36515 36614: gap of 100 bp
36615 37514: contig of 900 bp in length
37515 37614: gap of 100 bp
37615 38464: contig of 850 bp in length
38465 38564: gap of 100 bp
38565 39516: contig of 952 bp in length
39517 39616: gap of 100 bp
39617 40554: contig of 938 bp in length
40555 40654: gap of 100 bp
40655 41579: contig of 925 bp in length
41580 41679: gap of 100 bp
41680 42618: contig of 939 bp in length
42619 42718: gap of 100 bp
42719 43623: contig of 905 bp in length
43624 43723: gap of 100 bp
43724 44620: contig of 897 bp in length
44621 44720: gap of 100 bp
44721 45616: contig of 896 bp in length
45617 45716: gap of 100 bp
45717 46588: contig of 873 bp in length
46589 46689: gap of 100 bp
46690 47557: contig of 868 bp in length
47558 47657: gap of 100 bp
47658 48561: contig of 904 bp in length
48562 48661: gap of 100 bp
48662 49540: contig of 879 bp in length
49541 49640: gap of 100 bp

```

* 49641 50554: contig of 914 bp in length
* 50555 50654: gap of 100 bp
* 51567 51567: contig of 913 bp in length
* 51568 51667: gap of 100 bp
* 52525 52525: contig of 858 bp in length
* 52526 52625: gap of 100 bp
* 53517 53517: contig of 892 bp in length
* 53518 53617: gap of 100 bp
* 54506 54506: contig of 889 bp in length
* 54507 54606: gap of 100 bp
* 55490 55490: contig of 884 bp in length
* 55491 55590: gap of 100 bp
* 55432 55432: contig of 842 bp in length
* 56533 56533: gap of 100 bp
* 57403 57403: contig of 877 bp in length
* 57410 57509: gap of 100 bp
* 57510 58420: contig of 911 bp in length
* 58421 58520: gap of 100 bp
* 58521 59404: contig of 884 bp in length
* 59405 59504: gap of 100 bp
* 59505 60391: contig of 887 bp in length
* 60392 60491: gap of 100 bp
* 60492 61436: contig of 945 bp in length
* 61437 61536: gap of 100 bp
* 61537 62392: contig of 856 bp in length
* 62393 62492: gap of 100 bp
* 62493 63358: contig of 866 bp in length
* 63359 63458: gap of 100 bp
* 63459 64302: contig of 844 bp in length
* 64303 64402: gap of 100 bp
* 64403 65258: contig of 856 bp in length
* 65259 65358: gap of 100 bp
* 65359 66243: contig of 885 bp in length
* 66244 66343: gap of 100 bp
* 66344 67219: contig of 876 bp in length
* 67220 67319: gap of 100 bp
* 67320 68229: contig of 910 bp in length
* 68230 68329: gap of 100 bp
* 68330 69241: contig of 912 bp in length
* 69242 69341: gap of 100 bp
* 69342 70259: contig of 918 bp in length

```

Query Match 4.6%: Score 74; DB 76; Length 77313;
 Best Local Similarity 98.9%: Pred. No. 2e-30; Indels 0; Gaps 0;
 Matches 174; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Oy 1399 TCAGCTAGAAATCTGAGAGAGAAAGTCTGCTGCTGCTTACAGAGGTCATGCCATT 1458
|||||
Db 23073 TCAGCTAGAAATCTGAGAGAGAAAGTCTGCTGCTGCTTACAGAGGTCATGCCATT 23132
|||||
Oy 1459 CCGACCTTCACCAAGCTTAGAAGCCACATGATGTGGAAGCAGGTTGCTTCAAGATGT 1518
|||||
Db 23133 CCGACCTTCACCAAGCTTAGAAGCCACATGATGTGGAAGCAGGTTGCTTCAAGATGT 23192
|||||
Oy 1519 GTAGAGAGCTCTAATCTCTAGGAAGTGCCTTTAGGTCATCCAACTCTTT 1574
|||||
Db 23193 GTAGAGAGCTCTAATCTCTAGGAAGTGCCTTTAGGTCATCCAACTCTTT 23248
|||||

RESULT 23
LOCUS PIGMUOPR 1881 bp mRNA MAM 03-MAR-1999
DEFINITION Sus scrofa mu opioid receptor mRNA, complete cds.
ACCESSION L38645.1
VERSION L38645.1
KEYWORDS GI:2072391
SOURCE Sus scrofa
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 1881)
AUTHORS Pampusch,M.S., Osinski,M.A., Brown,D.R. and Mutaugh,M.P.
TITLE The porcine mu opioid receptor: molecular cloning and mRNA

```

JOURNAL distribution in lymphoid tissues
 MEDLINE J Neuroimmunol. 90 (2), 192-198 (1998)
 99032385.
 REFERENCE 2 (bases 1 to 1881)
 AUTHORS Osinski,M.A.
 TITLE Direct Submission
 JOURNAL Submitted (19-SEP-1996) Mark A. Osinski, Veterinary Pathobiology,
 University of Minnesota, St. Paul, MN 55108, USA
 COMMENT On May 6, 1997 this sequence version replaced gi:1553056.
 FEATURES
 source Location/Qualifiers
 1..1881
 /organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone="1d7"
 /tissue_type="cerebral cortex"
 /note="PCR amplified"
 237..1442
 /codon_start=1
 /product="mu opioid receptor"
 /protein_id="AA83770.1"
 /db_xref="GI:1553057"
 /translation="MDSADPRNANSGTDFSPSSMCSPPSPSSWVNFSLKGLSD
 PCIRNRTELGGSDSLCPGSPSWVATITMALYSIVGVGFENFLVMYIVATYK
 KTAATYIFNLADALATSTLPSPSYNLMGPFGLICKIVISIDYVMNFSIT
 LCTMSVRYLANVAVPVAIDPRPKNKIIINCMWISSAIGIPVMMATTKYNGSI
 DCAITFSPHTMYENLKLKICVFIFATFMPVLIITVCYGLMLRLKSRMSGKREKQ
 NLRITRMVAVVAVFVCMPIHIVIIALITIPETQTVSMHFCIALGYNSCL
 NPVLYAFIDEVFKRFREFCIPITSIIEOONSARIRONTDRHPSTANTVTRTNHLEN
 LEATPAFLP"

BASE COUNT 463 a 533 c 423 g 462 t
 ORIGIN

Query Match 4.4%: Score 71; DB 3; Length 1881;
 Best Local Similarity 100.0%: Pred. No. 1e-28;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 1238 AACCCAGTCCTTATGACATTTCTGATGATAAACTCAACGATGCTTAGAGAGTTCGT 1297
|||||
Db 1239 AACCCAGTCCTTATGACATTTCTGATGATAAACTCAACGATGCTTAGAGAGTTCGT 1298
|||||
Oy 1298 ATCCCACTC 1308
|||||
Db 1299 ATCCCACTC 1309
|||||

```

```

RESULT 24
LOCUS MMOR2 371 bp DNA ROD 08-NOV-1994
DEFINITION Mus musculus mu opioid receptor (MOR) gene, exon 2.
ACCESSION U10559
VERSION U10559.1
KEYWORDS GI:565066
SEGMENT 2 of 4
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 10 to 362)
AUTHORS Min,B.H., Augustin,L.B., Felsheim,R.F., Fuchs,J.A. and Loh,H.-H.
TITLE Genomic structure analysis of promoter sequence of a mouse mu
opioid receptor gene
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (19), 9081-9085 (1994)
MEDLINE 94377496.
REFERENCE 2 (bases 1 to 371)
AUTHORS Augustin,L.B.
TITLE Direct Submission
JOURNAL Submitted (13-JUN-1994) Lance B. Augustin, Pharmacology, University
of Minnesota, 435 Delaware Street SE, Minneapolis, MN 55455, USA
FEATURES
source Location/Qualifiers
1..371
/organism="Mus musculus"
/strain="C57 Black/6"

```

/db_xref="taxon:10090"
/clone="lambdamOR10"
/clone_lib="Stratagene Number 945301"
/tissue_type="liver"
/dev_stage="adult"
<1.9
/gene="MOR"
10.362
/gene="MOR"
/number=2
363.3371
/gene="MOR"
BASE COUNT 94 a 109 c 72 g 96 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 7.2e-22;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTGCTGCGAGATGCTTAGCCAC 597
Db 20 ATGAAGACTGCCACCAACATCTACATTTTCAACCTGCTGCGAGATGCTTAGCCAC 78

RESULT 25
AF074973 1334 bp mRNA ROD 31-AUG-1999
LOCUS Mus musculus mu oploid receptor MOR1D mRNA, alternatively spliced,
ACCESSION AF074973 complete cds.
VERSION AF074973.1 GI:5805152
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1334)
AUTHORS Pan,Y.X., Xu,J., Bolan,E., Abbadie,C., Chang,A., Zuckerman,A.,
Rossi,G. and Pasternak,G.W.
TITLE Identification and characterization of three new alternatively
spliced mu-oploid receptor isoforms
JOURNAL Mol. Pharmacol. 56 (2), 396-403 (1999)
MEDLINE 99348417
JOURNAL 2 (bases 1 to 1334)
MEDLINE 99348417
REFERENCE Pan,Y.-X., Xu,J., Wan,B.-L., Zuckerman,A.B., Rossi,G.C.,
Leventhal,L. and Pasternak,G.W.
TITLE Direct Submission
JOURNAL Submitted (29-JUN-1998) Neurology, Memorial Sloan-Kettering Cancer
Center, 1275 York Ave, New York, NY 10021, USA
FEATURES
source location/Qualifiers
1.1334
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
67.1248
/note="alternatively spliced exon 4"
/codon_start=1
/product="mu oploid receptor MOR1D"
/protein_id="A051861.1"
/db_xref="GI:5805153"
/translation="MDSAGAGNISDCSDPLAPASCSPPAGSWLNSHVGNOSDPG
PNRTGLGSHSLCQTPGSPMTATITMALYSIVCYVGLGFLNLYVIVYRMTKRA
TNYITFNALADALATSTLPFGSVNTLMGTWPGNLTCKIVISIDYNTSTFTICT
MSVDRIYAVCHPVKALDFRTPRNKIVNVCNWLSSAIGLPVFMATTKRGSIDCT
LTSHPITWENLKLICVFIFAFIMPLVITVCGMLILKLSVRMLSGSKERDNR
RIRRMVLVVAIVCVMTPIHIVIIKALITTEFTFOVSMHFCIALGYTNSCLNPV
LYAFIDENFRKCFRECIPTISSTIEONSARIRONTREHSTANTVDRTHORNEEPS
S"

BASE COUNT 320 a 397 c 297 g 320 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 7.3e-22;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTGCTGCGAGATGCTTAGCCAC 597
Db 361 ATGAAGACTGCCACCAACATCTACATTTTCAACCTGCTGCGAGATGCTTAGCCAC 419

RESULT 26
AF062753 1423 bp mRNA ROD 10-SEP-1999
LOCUS Mus musculus mu oploid receptor variant C mRNA, complete cds.
ACCESSION AF062753
VERSION AF062753.1 GI:5853308
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1423)
AUTHORS Pan,Y.X., Xu,J., Bolan,E., Abbadie,C., Chang,A., Zuckerman,A.,
Rossi,G. and Pasternak,G.W.
TITLE Identification and characterization of three new alternatively
spliced mu-oploid receptor isoforms
JOURNAL Mol. Pharmacol. 56 (2), 396-403 (1999)
MEDLINE 99348417
JOURNAL 2 (bases 1 to 1423)
REFERENCE Pan,Y.-X., Xu,J., Wan,B.-L., Zuckerman,A.B. and Pasternak,G.W.
AUTHORS Direct Submission
TITLE Submitted (04-MAY-1998) Department of Neurology, Memorial
Sloan-Kettering Cancer Center, 1275 York Ave., New York, NY 10021,
USA
FEATURES
source location/Qualifiers
1.1423
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
67.1383
/note="exon 4 splice variant; MOR-1C"
/codon_start=1
/product="mu oploid receptor variant C"
/protein_id="A054415.1"
/db_xref="GI:5853309"
/translation="MDSAGAGNISDCSDPLAPASCSPPAGSWLNSHVGNOSDPG
PNRTGLGSHSLCQTPGSPMTATITMALYSIVCYVGLGFLNLYVIVYRMTKRA
TNYITFNALADALATSTLPFGSVNTLMGTWPGNLTCKIVISIDYNTSTFTICT
MSVDRIYAVCHPVKALDFRTPRNKIVNVCNWLSSAIGLPVFMATTKRGSIDCT
LTSHPITWENLKLICVFIFAFIMPLVITVCGMLILKLSVRMLSGSKERDNR
RIRRMVLVVAIVCVMTPIHIVIIKALITTEFTFOVSMHFCIALGYTNSCLNPV
LYAFIDENFRKCFRECIPTISSTIEONSARIRONTREHSTANTVDRTHORNEEPS
VAOIFGTGYPPTVERKRCMKRMGRNLLPDGPRNOSSEGLGR"

BASE COUNT 343 a 423 c 317 g 340 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 7.3e-22;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTGCTGCGAGATGCTTAGCCAC 597
Db 361 ATGAAGACTGCCACCAACATCTACATTTTCAACCTGCTGCGAGATGCTTAGCCAC 419

RESULT 27
AF074974 1543 bp mRNA ROD 31-AUG-1999
LOCUS Mus musculus mu oploid receptor MOR1E mRNA, alternatively spliced,
ACCESSION AF074974 complete cds.
VERSION AF074974.1 GI:5805154
KEYWORDS

SOURCE	mouse mouse
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
AUTHORS	1 (bases 1 to 1543) Pan,Y.X., Xu,J., Bolan,E., Abbadie,C., Chang,A., Zuckerman,A., Rossi,G. and Pasternak,G.W.
TITLE	Identification and characterization of three new alternatively spliced mu opiod receptor isoforms
JOURNAL	Mol. Pharmacol. 56 (2), 396-403 (1999)
MEDLINE	99348417
REFERENCE	2 (bases 1 to 1543) Pan,Y.-X., Xu,J., Wan,B.-L., Zuckerman,A.B., Rossi,G.C., Leventhal,L. and Pasternak,G.W.
AUTHORS	Direct Submission Submitted (29-JUN-1998) Neurology, Memorial Sloan-Kettering Cancer Center, 1275 York Ave, New York, NY 10021, USA
TITLE	Location/Qualifiers
FEATURES	1..1543 /organism="Mus musculus" /strain="C57Bl/6J" /db_xref="taxon:10090" 67..1272 /note="alternatively spliced exon 4" /codon_start=1 /product="mu opiod receptor MOR1" /protein_id="A051862.1" /db_xref="GI:5805155" /translation="MSSAGPGENISDCDPLAPASCPAPSGMNLISHVGNOSDDPC PNTGGGSHSLCPOTGSPSMVATTATLALSYGVYLFENFLMYVIRYTKMKL TNIYNLALADLAISTIPROSVNITMGTFPGILCKIYISIDYNNMTSTIFTLCD MSDRIYACHPKALDFRTPNRNKIVNVCNMLISSAIGLVNMAATKTRQGSIDC LTFSHPTWENMLKICVFIFAFIMPVLIIVCYGLMLRLKSVMLSGSKEDRNRI RIIRMLVVAIVFICWPIHIIYIKLILIPETTFQTVSMHFCIALGTNSCLNLE LVAFLEKRCFRFCIPSTISIPQNSARIPQTRHPSTAVTVDRTHQKKLL QRCVDPHPV"
BASE COUNT	369 a 455 c 345 g 374 t
ORIGIN	
Query Match	3.7% Score 59; DB 12; Length 1543;
Best Local Similarity	100.0%; Pred. No. 7.4e-22;
Matches 59; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	539 ATGAAGACTGCACCAATCATCTATTTCAACCTTGCCTCTGGCAGATGCTTACGCAC 597 Db 361 ATGAAGACTGCACCAATCATCTATTTCAACCTTGCCTCTGGCAGATGCTTACGCAC 419
RESULT 28	
MMU26915	1610 bp mRNA ROD 09-NOV-1995
LOCUS	Mus musculus mu opiod receptor (MOR-1) mRNA, complete cds.
DEFINITION	U26915
ACCESSION	U26915.1 GI:1055230
VERSION	
KEYWORDS	house mouse.
SOURCE	Mus musculus
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
REFERENCE	1 (bases 1 to 1610) Rossi,G.C., Pan,Y.X., Brown,G.P. and Pasternak,G.W.
AUTHORS	Antisense mapping the MOR-1 opiod receptor: evidence for
TITLE	alternative splicing and a novel morphine-6 beta-glucuronide receptor
JOURNAL	FEBS Lett. 369 (2-3), 192-196 (1995)
MEDLINE	95377399
REFERENCE	2 (bases 1 to 1610) Pan,Y.-X.
AUTHORS	Direct Submission
TITLE	Submitted (11-MAY-1995) Ying-Xian Pan, Neurology, Memorial Sloan-Kettering Cancer Center, 1275 York Ave., New York, NY 10021, USA

FEATURES	Source	Location/Qualifiers
gene	CDS	1..1610 /organism="Mus musculus" /db_xref="taxon:10090" /tissue_type="brain" 283..1479 /gene="MOR-1" 283..1479 /gene="MOR-1" /codon_start=1 /product="mu opioid receptor" /protein_id="AA81170.1" /db_xref="GI:1055233"
BASE COUNT	373 a 476 c 368 g 393 t	
ORIGIN		ETADLP"
Query Match	3.7%; Score 59; DB 12; Length 1610;	
Best Local Similarity	100.0%; Pred. No. 7.4e-22;	
Matches 59; Conservative 0; Mismatches 0; Indels 0; Caps 0;		
Oy 539	ATGAGACTGCCACCAATCTACATTTTCAACCTGCTCGGAGATGCTTAGCCAC 597	
Db 577	ATGAAGACTGCACACMACATCTACATTTTCAACCTGCTCGGAGATGCTTAGCCAC 635	
RESULT 29		
LOCUS	AF167568	1729 bp mRNA ROD 28-JUN-2000
DEFINITION	Mus musculus mu opioid receptor variant F mRNA, complete cds.	
ACCESSION	AF167568	
VERSION	AF167568.1	GI:8778197
KEYWORDS		
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	Pan,Y.X., Xu,J., Bolan,E., Chang,A., Mahutler,L., Rossi,G. and Pasternak,G.W.	
TITLE	Isolation and expression of a novel alternatively spliced mu opioid receptor isoform, MOR-1F	
JOURNAL	FEBS Lett. 466 (2-3), 337-340 (2000)	
MEDLINE	20145060	
REFERENCE	2 (bases 1 to 1729)	
AUTHORS	Pan,Y.-X., Xu,J., Chang,A., Mahutler,L. and Pasternak,G.W.	
TITLE	Direct Submision	
JOURNAL	Submitted (13-JUN-2000) Neurology, Memorial Sloan-Kettering Cancer Center, 1275 York Ave., New York, NY 10021, USA	
FEATURES	Location/Qualifiers	
Source	1..1729	
	/organism="Mus musculus"	
	/strain="CD-1"	
	/db_xref="taxon:10090"	
	/chromosome="10"	
	/map="10A2"	
	67..1401	
	/note="MOR-1F: alternatively spliced variant of MOR-1 gene"	
	/codon_start=1	
	/product="mu opioid receptor variant F"	
	/protein_id="AA879213.1"	
	/db_xref="GI:8778198"	
	/translation="MDSSAGPGNISDCSDPLAPASCSPPAGSGWLNLSHYDGNQSDPCGPNRGLGSGSHSLCPQGTSPSMVAITITMALYSIVCVGLGNGFLVMYIVRYTKMTATNITIFMLADALATSTLPEFQSYNYLMGTWPGNLIKCKIVISIDYNMFTSIFLCTMSVRIYAVCHAPKVALDFEPPRNKIVNVCNMLISSAIGLPMVEMATTKYRQSIDCTLTSEHPYMWENMLIKCVFIEFAPFMPVLITTCVGMILRLKSVSMFGSGSKEDNRNRIITFMVAVVAVPIVCCTPIPHIYVITKALITPITPTQYMSWFCIALGCTNSCLNPLVALDENFRKCFERECIPTSTTEQDNSARIKRONTREHPTANTVDRIHQHOLEZETADLP"	

TRITYFENLADALATSTLPESQVNYLNGTPEFNGILCKIVISIDYNNMFTSITLCT
 MSVDRIYVCHPVKALDERTPNNAKIVNVCNMLSSAIGLPEPMATTKYRGSIDCT
 LTFSPHTWENLTKICVFIPAFIMPVILITTCYCLMTRKLSVNMSSKREKDNLR
 RTRMVLVVAVFIVCWTFPIHIVILKALITIPETFTIVSFCIALGYNISCLNPV
 LYAFIDENFKRCFREFCIPSTSIIEQNSARIQNTREHPTANVDRTHQAPACV
 LGANGQKASLDLLELETYSHQDAETNNGPYEGSKACPLAISIVPLT"
 BASE COUNT 417 a 505 c 395 g 412 t
 ORIGIN

Query Match 3.7%; Score 59; DB 12; Length 1729;
 Best Local Similarity 100.0%; Pred. No. 7.4e-22;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCGAGATGCTTAGCCAC 597
 DB 361 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCGAGATGCTTAGCCAC 419

RESULT 30
 LOCUS A68824 2229 bp DNA PAT 06-MAY-1999
 DEFINITION Sequence 1 from Patent WO9802534.
 ACCESSION A68824
 VERSION A68824.1 GI:4759752
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 2229)
 Kieffer, B.L., Matthes, H.W., Simonin, F.H., Dierich, A. and Lemeur, M.
 TRANSGENIC ANIMAL WHOSE EXPRESSION OF THE OPIATE RECEPTORS IS
 MODIFIED
 JOURNAL Patent: WO 9802534-A-22-JAN-1998;
 CENTRE NAT RECH SCIENT (FR)
 Other publication FR 2750825 19980116.
 COMMENT Location/Qualifiers
 FEATURES
 source 1..2229
 /organism="unidentified"
 /db_xref="taxon:32644"
 /note="unidentified protein product"
 /codon_start=1
 /protein_id="CAB42460.1"
 /db_xref="GI:4759753"
 /translation="MDSAGSGNISDCSDPLAPASWSPAPSGMNLSHVDGNOSDPCG
 PNRTGLGSHSLCPOTGSPSMYTAITIALTSIVCYVGLFENFLVMYIVYRTKRTA
 TNITFNLADALATSTLPESQVNYLNGTPEFNGILCKIVISIDYNNMFTSITLCT
 MSVDRIYVCHPVKALDERTPNNAKIVNVCNMLSSAIGLPEPMATTKYRGSIDCT
 LTFSPHTWENLTKICVFIPAFIMPVILITTCYCLMTRKLSVNMSSKREKDNLR
 RTRMVLVVAVFIVCWTFPIHIVILKALITIPETFTIVSFCIALGYNISCLNPV
 LYAFIDENFKRCFREFCIPSTSIIEQNSARIQNTREHPTANVDRTHQAPACV
 ETAPLP"

CDS
 BASE COUNT 562 a 608 c 489 g 570 t
 ORIGIN

Query Match 3.7%; Score 59; DB 5; Length 2229;
 Best Local Similarity 100.0%; Pred. No. 7.4e-22;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCGAGATGCTTAGCCAC 597
 DB 550 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCGAGATGCTTAGCCAC 608

RESULT 31
 LOCUS MMU19380 2229 bp mRNA ROD 07-FEB-1996
 DEFINITION Mus musculus mu opioid receptor cDNA, complete cds.
 ACCESSION U19380
 VERSION U19380.1 GI:885864
 KEYWORDS

SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 2229)
 Kauffman, D.L., Keith, D.E., Anton, B., Tian, J., Magendzo, K.,
 Newman, D.J., Tran, T., Lee, D.S., Wen, C., Xia, Y., Lussis, A.J. and
 Evans, C.J.
 TITLE Characterization of the murine mu opioid receptor gene
 JOURNAL J. Biol. Chem. 270 (26), 15877-15883 (1995)
 MEDLINE 95318184
 REFERENCE 2 (bases 1 to 2229)
 Evans, C.C.
 TITLE Direct Submission
 JOURNAL Submitted (04-JAN-1995) Christopher J Evans, Psychiatry and
 Biobehavioral Sciences, University of California at Los Angeles,
 UCLA-NPI, 760 Westwood Plaza, Los Angeles, CA 90024-1759, USA
 FEATURES
 source 1..2229
 /organism="Mus musculus"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="tmOR"
 /tissue_type="brain"
 /dev_stage="adult"
 /note="in lambda gt10"
 256..1452
 /codon_start=1
 /product="mu opioid receptor"
 /protein_id="AA68878.1"
 /db_xref="GI:885865"
 /translation="MDSAGSGNISDCSDPLAPASWSPAPSGMNLSHVDGNOSDPCG
 PNRTGLGSHSLCPOTGSPSMYTAITIALTSIVCYVGLFENFLVMYIVYRTKRTA
 TNITFNLADALATSTLPESQVNYLNGTPEFNGILCKIVISIDYNNMFTSITLCT
 MSVDRIYVCHPVKALDERTPNNAKIVNVCNMLSSAIGLPEPMATTKYRGSIDCT
 LTFSPHTWENLTKICVFIPAFIMPVILITTCYCLMTRKLSVNMSSKREKDNLR
 RTRMVLVVAVFIVCWTFPIHIVILKALITIPETFTIVSFCIALGYNISCLNPV
 LYAFIDENFKRCFREFCIPSTSIIEQNSARIQNTREHPTANVDRTHQAPACV
 ETAPLP"

CDS

BASE COUNT 562 a 608 c 489 g 570 t
 ORIGIN

Query Match 3.7%; Score 59; DB 12; Length 2229;
 Best Local Similarity 100.0%; Pred. No. 7.4e-22;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCGAGATGCTTAGCCAC 597
 DB 550 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCGAGATGCTTAGCCAC 608

RESULT 32
 LOCUS AC055776 178454 bp DNA HTG 22-JUL-2000
 DEFINITION Mus musculus chromosome 10 clone RP23-11015 map 10, WORKING DRAFT
 SEQUENCE, 21 unordered pieces.
 ACCESSION AC055776
 VERSION AC055776.2 GI:9369492
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 178454)
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE Mus musculus chromosome 10, clone RP23-11015
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 178454)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
 Boguslavsky, L., Bouckgalter, B., Brown, A., Burkett, G.,
 Campolano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,

TITLE
JOURNAL
COMMENT

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heatford, A., Horton, L.,
Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Larocque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Liu, G., Liu, G., Locke, K., MacDonald, P., Margulis, N.,
McCarthy, M., McEwan, P., McGuck, A., McKernan, K., McPheeters, R.,
Meldrum, J., Menus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Olyar, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, D., Turrell, A., Travers, M., Triggillo, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (18-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 22, 2000 this sequence version replaced g1:7382600.

All repeats were identified using RepeatMasker:

Slit, A. F. A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L5745

Center clone name: 11.O.15

Summary Statistics

Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 166586 bases at least Q40
Consensus quality: 172885 bases at least Q30
Consensus quality: 175270 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 176454; sum-of-ctrls
Quality coverage: 4.5 in Q20 bases; agarose-fp
Quality coverage: 4.8 in Q20 bases; sum-of-ctrls

NOTE: This is a 'working draft' sequence. It currently
consists of 21 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 1545: contig of 1545 bp in length
1546 1645: gap of 100 bp
1646 2950: contig of 1305 bp in length
2951 3050: gap of 100 bp
3051 5112: contig of 2062 bp in length
5113 5212: gap of 100 bp
5213 8232: contig of 3020 bp in length
8233 8332: gap of 100 bp
8333 13079: contig of 4747 bp in length
13080 13179: gap of 100 bp
13180 16940: contig of 3761 bp in length
16941 17040: gap of 100 bp
17041 21192: contig of 4152 bp in length
21193 21292: gap of 100 bp
21293 26578: contig of 5286 bp in length
26579 26678: gap of 100 bp
26679 32608: contig of 5930 bp in length
32609 32708: gap of 100 bp
32709 38888: contig of 6180 bp in length
38889 38988: gap of 100 bp
38989 44556: contig of 5568 bp in length

FEATURES

source

* 44557 44656: gap of 100 bp
* 44657 51768: contig of 7112 bp in length
* 51769 51868: gap of 100 bp
* 51869 58681: contig of 6813 bp in length
* 58682 58781: gap of 100 bp
* 58782 65622: contig of 6841 bp in length
* 65623 65722: gap of 100 bp
* 65723 77537: contig of 11815 bp in length
* 77538 77637: gap of 100 bp
* 77638 85102: contig of 7465 bp in length
* 85103 85202: gap of 100 bp
* 85203 99219: contig of 14017 bp in length
* 99220 99319: gap of 100 bp
* 99320 110888: contig of 11570 bp in length
* 110889 110989: gap of 100 bp
* 110990 132713: contig of 21724 bp in length
* 132714 132813: gap of 100 bp
* 132814 152788: contig of 19975 bp in length
* 152789 152888: gap of 100 bp
* 152889 178454: contig of 25566 bp in length.
Location/Qualifiers
1. 178454
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="10"
/map="10"
/clone="RP23-11015"
/clone_lib="RPCI-23 Female Mouse BAC"
1. 1545
/note="assembly-fragment"
1646 2950
/note="assembly-fragment"
3051 5112
/note="assembly-fragment"
5213 8232
/note="assembly-fragment"
8333 13079
/note="assembly-fragment"
13180 16940
/note="assembly-fragment"
17041 21192
/note="assembly-fragment"
21293 26578
/note="assembly-fragment"
26679 32608
/note="assembly-fragment"
32709 38888
/note="assembly-fragment"
38989 44556
/note="assembly-fragment"
vector_side:right
clone_end:17
44657 51768
/note="assembly-fragment"
51869 58681
/note="assembly-fragment"
58782 65622
/note="assembly-fragment"
65723 77537
/note="assembly-fragment"
77638 85102
/note="assembly-fragment"
85203 99219
/note="assembly-fragment"
99320 110889
/note="assembly-fragment"
110990 132713
/note="assembly-fragment"
132814 152788
/note="assembly-fragment"
clone_end:SP6
vector_side:left
152889 178454
misc_feature

```

/note="assembly_fragment"
BASE COUNT      52031 a 35300 c 36144 g 52974 t 2005 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 7.9e-22;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTCTGGCAGATGCTTACCCAC 597
|||||
Db 60871 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTCTGGCAGATGCTTACCCAC 60929

RESULT 33
AF266480 193 bp mRNA MAM 19-JUN-2000
LOCUS
DEFINITION Ovis aries mu oploid receptor mRNA, partial cds.
ACCESSION AF266480
VERSION AF266480.1 GI:8572232
KEYWORDS
SOURCE
ORGANISM sheep.
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 193)
Thompson, R.C.
REFERENCE
AUTHORS Thompson, R.C.
TITLE Ovine Mu Oploid Receptor
JOURNAL Unpublished
REFERENCE
AUTHORS Thompson, R.C.
TITLE 2 (bases 1 to 193)
JOURNAL Direct Submission
Submitted (10-MAY-2000) Psychiatry, University of Michigan, 4451
Kresge I, Ann Arbor, MI 48109-0512, USA

FEATURES
Source
Location/Qualifiers
1..193
/organism="Ovis aries"
/db_xref="taxon:9940"
<1..>193
/codon_start=3
/product="mu oploid receptor"
/protein_id="AA77054.1"
/db_xref="GI:8572233"
/translation="NVVPIILITVCYGMILRLKSVYMLSGSKEDRNLRITRMVLV
VVAVFVVCWPIHPIFVIVW"

BASE COUNT      42 a 45 c 54 g 52 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1016 CGCCTCAAGACTGCCACATCTCTGCTGCCAAGAAAGACAGGAA 1065
|||||
Db 54 CGCCTCAAGACTGCCACATCTCTGCTGCCAAGAAAGACAGGAA 103

RESULT 34
AC022855 77313 bp DNA HTG 13-JUL-2000
LOCUS
DEFINITION Homo sapiens chromosome 11 clone RP11-310M4 map 11, LOW-PASS
SEQUENCE SAMPLING.
ACCESSION AC022855
VERSION AC022855.2 GI:9158694
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 77313)
REFERENCE
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
Homo sapiens chromosome 11, clone RP11-310M4
Unpublished
2 (bases 1 to 77313)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choelel, Y., Collangelo, M., Collins, S., Collymore, A., Cooke, P.,
Darellano, K., Dewar, K., Domino, M., Doyle, M., Fensholt, J.,
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lebecky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
McPherson, R., Meldrum, J., Meneses, L., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K.,
Pierre, N., Pisanu, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, R., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talmes, J., Teste, S., Theodore, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
Zimmer, A. and Zody, M.

Direct Submission
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6922183.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WtBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L6117
Center clone name: 310_M4

* NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1
876 975: contig of 875 bp in length
876 975: gap of 100 bp
976 1889: contig of 914 bp in length
1890 1989: gap of 100 bp
1990 2894: contig of 905 bp in length
2895 2994: gap of 100 bp
2995 3861: contig of 867 bp in length
3862 3961: gap of 100 bp
3962 4832: contig of 871 bp in length
4833 4932: gap of 100 bp
4933 5840: contig of 908 bp in length
5841 5940: gap of 100 bp
5941 6823: contig of 883 bp in length
6824 6923: gap of 100 bp
6924 7830: contig of 907 bp in length
7831 7930: gap of 100 bp
7931 8844: contig of 914 bp in length
8845 8944: gap of 100 bp
8945 9870: contig of 926 bp in length
9871 9970: gap of 100 bp
9971 10835: contig of 865 bp in length
10836 10935: gap of 100 bp
10936 11840: contig of 905 bp in length
11841 11940: gap of 100 bp
11941 12816: contig of 876 bp in length
12817 12916: gap of 100 bp

```

```

* 12917 13799: contig of 883 bp in length
* 13800 13899: gap of 100 bp
* 13900 14784: contig of 885 bp in length
* 14785 14884: gap of 100 bp
* 14885 15776: contig of 892 bp in length
* 15777 15876: gap of 100 bp
* 15877 16773: contig of 897 bp in length
* 16774 16873: gap of 100 bp
* 16874 17772: contig of 889 bp in length
* 17773 17872: gap of 100 bp
* 17873 18790: contig of 918 bp in length
* 18791 18890: gap of 100 bp
* 18891 19745: contig of 855 bp in length
* 19746 19845: gap of 100 bp
* 19846 20749: contig of 904 bp in length
* 20750 20849: gap of 100 bp
* 20850 21718: contig of 869 bp in length
* 21719 21818: gap of 100 bp
* 21819 22692: contig of 874 bp in length
* 22693 22792: gap of 100 bp
* 22793 23653: contig of 861 bp in length
* 23654 23753: gap of 100 bp
* 23754 24629: contig of 876 bp in length
* 24630 24729: gap of 100 bp
* 24730 25603: contig of 874 bp in length
* 25604 25703: gap of 100 bp
* 25704 26550: contig of 847 bp in length
* 26551 26650: gap of 100 bp
* 26651 27562: contig of 912 bp in length
* 27563 27662: gap of 100 bp
* 27663 28573: contig of 911 bp in length
* 28574 28673: gap of 100 bp
* 28674 29587: contig of 914 bp in length
* 29588 29687: gap of 100 bp
* 29688 30564: contig of 877 bp in length
* 30565 30664: gap of 100 bp
* 30665 31568: contig of 904 bp in length
* 31569 31668: gap of 100 bp
* 31669 32538: contig of 870 bp in length
* 32539 32638: gap of 100 bp
* 32639 33543: contig of 905 bp in length
* 33544 33643: gap of 100 bp
* 33644 34549: contig of 906 bp in length
* 34550 34649: gap of 100 bp
* 34650 35551: contig of 902 bp in length
* 35552 35651: gap of 100 bp
* 35652 36514: contig of 863 bp in length
* 36515 36614: gap of 100 bp
* 36615 37514: contig of 900 bp in length
* 37515 37614: gap of 100 bp
* 37615 38464: contig of 850 bp in length
* 38465 38564: gap of 100 bp
* 38565 39516: contig of 952 bp in length
* 39517 39616: gap of 100 bp
* 39617 40554: contig of 938 bp in length
* 40555 40654: gap of 100 bp
* 40655 41579: contig of 925 bp in length
* 41580 41679: gap of 100 bp
* 41680 42618: contig of 939 bp in length
* 42619 42718: gap of 100 bp
* 42719 43623: contig of 905 bp in length
* 43624 43723: gap of 100 bp
* 43724 44620: contig of 897 bp in length
* 44621 44720: gap of 100 bp
* 44721 45616: contig of 896 bp in length
* 45617 45716: gap of 100 bp
* 45717 46589: contig of 873 bp in length
* 46590 46689: gap of 100 bp
* 46690 47557: contig of 868 bp in length
* 47558 47657: gap of 100 bp
* 47658 48561: contig of 904 bp in length
* 48562 48661: gap of 100 bp
* 48662 49540: contig of 879 bp in length

```

```

* 49541 49640: gap of 100 bp
* 49641 50554: contig of 914 bp in length
* 50555 50654: gap of 100 bp
* 50655 51567: contig of 913 bp in length
* 51568 51667: gap of 100 bp
* 51668 52525: contig of 858 bp in length
* 52526 52625: gap of 100 bp
* 52626 53517: contig of 892 bp in length
* 53518 53617: gap of 100 bp
* 53618 54506: contig of 889 bp in length
* 54507 54606: gap of 100 bp
* 54607 55490: contig of 884 bp in length
* 55491 55590: gap of 100 bp
* 55591 56432: contig of 842 bp in length
* 56433 56532: gap of 100 bp
* 56533 57409: contig of 877 bp in length
* 57410 57509: gap of 100 bp
* 57510 58420: contig of 911 bp in length
* 58421 58520: gap of 100 bp
* 58521 59404: contig of 884 bp in length
* 59405 59504: gap of 100 bp
* 59505 60391: contig of 887 bp in length
* 60392 60491: gap of 100 bp
* 60492 61436: contig of 945 bp in length
* 61437 61536: gap of 100 bp
* 61537 62392: contig of 856 bp in length
* 62393 62492: gap of 100 bp
* 62493 63358: contig of 866 bp in length
* 63359 63458: gap of 100 bp
* 63459 64302: contig of 844 bp in length
* 64303 64402: gap of 100 bp
* 64403 65258: contig of 856 bp in length
* 65259 65358: gap of 100 bp
* 65359 66243: contig of 885 bp in length
* 66244 66343: gap of 100 bp
* 66344 67219: contig of 876 bp in length
* 67220 67319: gap of 100 bp
* 67320 68229: contig of 910 bp in length
* 68230 68328: gap of 100 bp
* 68330 69241: contig of 912 bp in length
* 69242 69341: gap of 100 bp
* 69342 70259: contig of 918 bp in length

Query Match      3.0%: Score 49; DB 76; Length 77313;
Best Local Similarity 100.0%: Pred. No. 4,1e-16;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1425 CTGCTCCGTTCCCTACAGAGGTCATGCATTCGACCTTACACGAG 1473
    |||||
Db 40745 CTGCTCCGTTCCCTACAGAGGTCATGCATTCGACCTTACACGAG 40697

RESULT 35
RNU35424      1367 bp      mRNA      ROD      12-OCT-1995
LOCUS        Rattus norvegicus mu opioid receptor mRNA, complete cds.
DEFINITION   U35424
ACCESSION    U35424
VERSION      U35424.1 GI:1017731
SOURCE
  ORGANISM   Norway rat.
              Rattus norvegicus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
              Rattus.
REFERENCE    1 (bases 1 to 1367)
              Zastawny,R.L., George,S.R., Nguyen,T., Cheng,R., Tsatsos,J.,
AUTHORS      Briones-Jrblna,R. and O'Dowd,B.F.
              Cloning, characterization, and distribution of a mu-opioid receptor
              in rat brain
JOURNAL      J. Neurochem. 62 (6), 2099-2105 (1994)
MEDLINE      94246380
REFERENCE    2 (bases 1 to 1367)
              O'Dowd,B.F.
AUTHORS

```

TITLE Direct Submission
JOURNAL Submitted (05-SEP-1995) Brian F. O'Dowd, Pharmacology, University
of Toronto, 8 Taddle Creek Rd., Toronto, ON M5S 1A8, Canada

FEATURES
Source
Location/Qualifiers
1. 1367
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
70. 1266
/codon_start=1
/product="mu opioid receptor"
/protein_id="AA09180.1"
/translation="MDSSTGPGNTSDCSDPLAQSAPSPAGSMNLNLSHYDNGSDPCG
LNRTGLGNDSLCPQTSPPSWATITTAALYSIVCVGLFNGFLVMYIVRYTKMKA
TNITFNLADALATSTLPQSVNYLMGTWPEFTILCKIVISIDYNNKFSITFLCT
MSVDRYAVCHPVKALDPRTPRNKIVNVCWMLISSAIGLPSVMAATKRGOSIDCT
LTFSPHTWENLKLICVETFAFIMPVLIITVCGMLRLKSVMLSGSKEDNRL
RITRMVLVVAVFVTCWPIHIVIKALITIPETFEQVSMHCIALGYNSCLNPV
LYAFIDENFKRCFREFCIPSTIEQNSTVRONTREHPSSTANTVDRTNQLENLEA
ETAPLP"

CDS
170. 1366
/tissue_type="olfactory bulb"
/tissue_1bp="lambda ZAP1 from Stratagene"
/codon_start=1
/product="mu opioid receptor"
/protein_id="AA16075.1"
/db_xref="GI:437672"
/translation="MDSSTGPGNTSDCSDPLAQSAPSPAGSMNLNLSHYDNGSDPCG
LNRTGLGNDSLCPQTSPPSWATITTAALYSIVCVGLFNGFLVMYIVRYTKMKA
TNITFNLADALATSTLPQSVNYLMGTWPEFTILCKIVISIDYNNKFSITFLCT
MSVDRYAVCHPVKALDPRTPRNKIVNVCWMLISSAIGLPSVMAATKRGOSIDCT
LTFSPHTWENLKLICVETFAFIMPVLIITVCGMLRLKSVMLSGSKEDNRL
RITRMVLVVAVFVTCWPIHIVIKALITIPETFEQVSMHCIALGYNSCLNPV
LYAFIDENFKRCFREFCIPSTIEQNSTVRONTREHPSSTANTVDRTNQLENLEA
ETAPLP"

BASE COUNT 330 a 434 c 312 g 325 t

Query Match 2.9%; Score 47; DB 12; Length 1367;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGA 585
|||||
DB 364 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGA 410
|||||

RESULT 36
RATMOP10D 1401 bp mRNA ROD 24-JAN-1994
LOCUS Rat mu opioid receptor mRNA, complete cds.
DEFINITION L22455
ACCESSION L22455
VERSION L22455.1 GI:437671
KEYWORDS mu opioid receptor.
SOURCE Rattus norvegicus (strain Sprague-Dawley) cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1401)
Thompson, R.C., Mansour, A., Akil, H. and Watson, S.J.
Cloning and pharmacological characterization of a rat mu opioid
receptor
Neuron 11 (5), 903-913 (1993)
94059560
Location/Qualifiers
1. 1401
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/sex="male"
/tissue_type="olfactory bulb"
/tissue_1bp="lambda ZAP1 from Stratagene"
/codon_start=1
/product="mu opioid receptor"
/protein_id="AA16075.1"
/db_xref="GI:437672"
/translation="MDSSTGPGNTSDCSDPLAQSAPSPAGSMNLNLSHYDNGSDPCG
LNRTGLGNDSLCPQTSPPSWATITTAALYSIVCVGLFNGFLVMYIVRYTKMKA
TNITFNLADALATSTLPQSVNYLMGTWPEFTILCKIVISIDYNNKFSITFLCT
MSVDRYAVCHPVKALDPRTPRNKIVNVCWMLISSAIGLPSVMAATKRGOSIDCT
LTFSPHTWENLKLICVETFAFIMPVLIITVCGMLRLKSVMLSGSKEDNRL
RITRMVLVVAVFVTCWPIHIVIKALITIPETFEQVSMHCIALGYNSCLNPV
LYAFIDENFKRCFREFCIPSTIEQNSTVRONTREHPSSTANTVDRTNQLENLEA
ETAPLP"

BASE COUNT 330 a 434 c 312 g 325 t

ORIGIN
Query Match 2.9%; Score 47; DB 12; Length 1401;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGA 585
|||||
DB 464 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGA 510
|||||

RESULT 37
RNU02083 1448 bp mRNA ROD 20-JUL-1995
LOCUS Rattus norvegicus mu-opioid receptor mRNA, complete cds.
DEFINITION U02083
ACCESSION U02083
VERSION U02083.1 GI:403573
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1448)
Bunzow, J.R., Zhang, G., Bouvier, C., Saez, C., Ronnekleiv, O.K.,
Kelly, M.J. and Grandy, D.K.
Characterization and distribution of a cloned rat mu-opioid
receptor
J. Neurochem. 64 (1), 14-24 (1995)
95096825
2 (bases 1 to 1448)
Bunzow, J.R.
Direct Submission
Submitted (24-SEP-1993) James R. Bunzow, VIABR, Oregon Health
Sciences University, 3181 S.W. Sam Jackson Park Rd., Portland, OR
97201 USA
Location/Qualifiers
1. 1448
/organism="Rattus norvegicus"
/strain="Sprague Dawley"
/db_xref="taxon:10116"
211. 1407
/codon_start=1
/product="mu-opioid receptor"
/protein_id="AA070049.1"
/db_xref="GI:403574"
/translation="MDSSTGPGNTSDCSDPLAQSAPSPAGSMNLNLSHYDNGSDPCG
LNRTGLGNDSLCPQTSPPSWATITTAALYSIVCVGLFNGFLVMYIVRYTKMKA
TNITFNLADALATSTLPQSVNYLMGTWPEFTILCKIVISIDYNNKFSITFLCT
MSVDRYAVCHPVKALDPRTPRNKIVNVCWMLISSAIGLPSVMAATKRGOSIDCT
LTFSPHTWENLKLICVETFAFIMPVLIITVCGMLRLKSVMLSGSKEDNRL
RITRMVLVVAVFVTCWPIHIVIKALITIPETFEQVSMHCIALGYNSCLNPV
LYAFIDENFKRCFREFCIPSTIEQNSTVRONTREHPSSTANTVDRTNQLENLEA
ETAPLP"

BASE COUNT 345 a 443 c 326 g 334 t

Query Match 2.9%; Score 47; DB 12; Length 1448;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGA 585
|||||
DB 505 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGA 551
|||||

RESULT 38
RATMORA 1586 bp mRNA ROD 04-AUG-1993
LOCUS Rattus norvegicus mu opioid receptor mRNA, complete cds.
DEFINITION L13069
ACCESSION


```

/codon_start=1
/product="rat opioid receptor B"
/db_xref="GI:391867"
/translation="MDSSTSPGNTSDCSDFLAAGSCSPAFGSMNLINSHVDGNSDPG
LNTGIGDNDLCPOTGSPSMVAITITMALSYVYGLGNEFLVMYIVRYRMKA
TNYIFENIALADALATSTLPGSYNYVMWPGTILCKIVISIDYNYMTSIFLCT
MSYDRYAVCHPKALDEPRIPRNKIVNVMNLISALIGPMVMATTKYRROSDICT
LTPSHPMWENELTKICVFPFAPMPVLTITCYGSMILKLGVMISGSKERDRNR
RTRRMVLVAVIVCTPPIHIYIKALITTEPTTQYTSMEFCIALGTTNSCLNRY
LVAFDENFRFCREFCIPSTIEQNSYRVRONTREHPSSTANTYDRINHOLENLEA
ETAPLP"
BASE COUNT      614 a      650 c      506 g      627 t
ORIGIN

Query Match      2.98; Score 47; DB 12; Length 2397;
Best Local Similarity 100.0%; Pred. No. 5.4e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAGACTGCCACACATCTACATTTCAACCTGCTGGCAGA 585
Db 478 ATGAGACTGCCACACATCTACATTTCAACCTGCTGGCAGA 524

RESULT 41
LOCUS      S77863      720 bp      mRNA      ROD      26-SEP-1995
DEFINITION mu-opioid receptor MOR [rats, peritoneal macrophages, mRNA Partial,
720 nt].
ACCESSION  S77863
VERSION     S77863.1 GI:998526
KEYWORDS
SOURCE
ORGANISM
Rattus sp. peritoneal macrophages.
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 720)
Sedq,M., Roy,S., Ramakrishnan,S., Elde,R. and Loh,H.H.
Complementary DNA Cloning of a mu-opioid receptor from rat
peritoneal macrophages
Biochem. Biophys. Res. Commun. 209 (2), 563-574 (1995)
JOURNAL
MEDLINE
95251654
Genbank staff at the National Library of Medicine created this
entry [NCBI gidsq 166498] from the original journal article.
This sequence comes from Fig. 3.
FEATURES
Source
Location/Qualifiers
1..720
/organism="Rattus sp."
/db_xref="taxon:10118"
1..720
/partial
/gene="mu-opioid receptor MOR"
BASE COUNT      168 a      221 c      144 g      187 t
ORIGIN

Query Match      2.58; Score 41; DB 12; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 545 ACTGCACCAACATCTACATTTCAACCTGCTGGCAGA 585
Db 1 ACTGCACCAACATCTACATTTCAACCTGCTGGCAGA 41

RESULT 42
LOCUS      CPU67928      354 bp      DNA      ROD      02-JAN-1997
DEFINITION Cavia porcellus mu-opioid receptor gene, partial cds.
ACCESSION  U67928
VERSION     U67928.1 GI:1763012

```

```

KEYWORDS
SOURCE
ORGANISM
Cavia porcellus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hysticognathi; Cavidae; Cavia.
REFERENCE
AUTHORS
Ronnkleiv,O.K., Bosch,M.A., Cunningham,M.J., Wagner,E.J.,
Grandy,D.K. and Kelly,M.J.
Down regulation of mu-opioid receptor mRNA in the medobasal
hypothalamus of the female guinea pig following morphine treatment
Unpublished
2 (bases 1 to 354)
Grandy,D.K.
Direct Submission
Submitted (25-AUG-1996) Vollum Institute, 3181 S.W. Sam Jackson
Park Rd., Portland, OR 97201, USA
1..354
Location/Qualifiers
1..354
/organism="Cavia porcellus"
/db_xref="taxon:10141"
<1..59
/number=1
<60..>354
/codon_start=2
/product="mu-opioid receptor"
/db_xref="GI:1763013"
/translation="YTKMTATNITYFENIALADALATSTLPGSYNYVMWPGTIL
CKIVISIDYNYMTSIFLCTMSYDRYAVCHPKALDEPRIPRNKIVNVMNLISALIGPMVMATTKYRROSDICT
LTPSHPMWENELTKICVFPFAPMPVLTITCYGSMILKLGVMISGSKERDRNR
RTRRMVLVAVIVCTPPIHIYIKALITTEPTTQYTSMEFCIALGTTNSCLNRY
LVAFDENFRFCREFCIPSTIEQNSYRVRONTREHPSSTANTYDRINHOLENLEA
ETAPLP"
BASE COUNT      91 a      98 c      60 g      105 t
ORIGIN

Query Match      2.48; Score 38; DB 12; Length 354;
Best Local Similarity 100.0%; Pred. No. 7.4e-10;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 557 ATCTACATTTCAACCTGCTGGCAGATGCTTAC 594
Db 88 ATCTACATTTCAACCTGCTGGCAGATGCTTAC 125

RESULT 43
LOCUS      S79903      1944 bp      DNA      ROD      17-FEB-1996
DEFINITION mu opioid receptor [exon 1, promoter] [rats, Genomic, 1944 nt].
ACCESSION  S79903
VERSION     S79903.1 GI:119532
KEYWORDS
SOURCE
ORGANISM
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1944)
Kraus,J., Horn,G., Zimprich,A., Simon,T., Mayer,P. and Holt,V.
Molecular cloning and functional analysis of the rat mu opioid
receptor gene promoter
Biochem. Biophys. Res. Commun. 215 (2), 591-597 (1995)
JOURNAL
MEDLINE
96011819
Genbank staff at the National Library of Medicine created this
entry [NCBI gidsq 172339] from the original journal article.
This sequence comes from Fig. 1.
Location/Qualifiers
1..1944
/organism="Rattus sp."
/db_xref="taxon:10118"
FEATURES
Source

```

mRNA 1361. >1944
gene 1661. 1944

BASE COUNT 498 a 468 c 446 g 532 t
ORIGIN

Query Match 2.28; Score 35; DB 12; Length 1944;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 491 CTCTCGAACTTCCGTCATGTATGATGCT 525
Db 1907 CTCTCGAACTTCCGTCATGTATGATGCT 1941

Search completed: November 14, 2000, 23:48:26
Job time: 7524 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2000, 22:43:22 ; Search time 86.83 Seconds
(without alignments)
6965.529 Million cell updates/sec

Title: US-08-305-518-7

Perfect score: 1610
Sequence: 1 CGGATGACCCTCTGCACT.....GCTCTGCACATTAGAGCCG 1610

Scoring table: OLIGO_MUC
Gapop 60.0 , Gapext 60.0

Searched: 480022 seqs, 187831343 residues

Word size : 35

Total number of hits satisfying chosen parameters: 33

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

N_Geneseq_36:*

1:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20:	/cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21:	/cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1610	100.0	1610	089226	Human mu oploid re
2	1256	78.0	2162	19 V61984	Human mu-oploid re
3	1256	78.0	2162	19 V61995	Human mu-oploid re
4	1240	77.0	2160	16 093102	Human mu opiate re
5	1240	77.0	2162	21 288470	Human mu oploid re
6	1215	75.5	2162	19 V61985	Human mu-oploid re
7	1205	74.8	2162	19 V61986	Human mu-oploid re
8	1205	74.8	2162	19 V61987	Human mu-oploid re
9	1205	74.8	2162	19 V61988	Human mu-oploid re
10	1205	74.8	2162	19 V61989	Human mu-oploid re
11	1205	74.8	2162	19 V61990	Human mu-oploid re
12	1205	74.8	2162	19 V61991	Human mu-oploid re

13	1205	74.8	2162	19 V61992	Human mu-oploid re
14	1205	74.8	2162	19 V61993	Human mu-oploid re
15	1205	74.8	2162	19 V61994	Human mu-oploid re
16	441	27.4	441	20 X59781	DNA encoding a mu3
17	392	24.3	829	15 Q56703	Partial sequence o
18	59	3.7	268	21 260733	Murine mu-oploid r
19	59	3.7	1238	21 260727	CDNA encoding mur1
20	59	3.7	1257	21 260730	CDNA encoding mur1
21	59	3.7	1334	21 260728	CDNA encoding mur1
22	59	3.7	1346	21 260737	CDNA encoding mur1
23	59	3.7	1365	21 260736	CDNA encoding mur1
24	59	3.7	1423	21 260726	CDNA encoding mur1
25	59	3.7	1542	21 260729	CDNA encoding mur1
26	59	3.7	1610	21 260741	CDNA encoding mur1
27	59	3.7	1729	21 260734	CDNA encoding mur1
28	59	3.7	1981	15 Q56705	Partial sequence o
29	59	3.7	2045	21 260735	CDNA encoding mur1
30	59	3.7	2229	19 V49252	Mouse mu opiate re
31	47	2.9	1618	16 089222	Rat mu oploid rece
32	47	2.9	1618	16 089223	Transcription regu
33	47	2.9	2070	15 Q79199	Rat mu-subtype opi

ALIGNMENTS

RESULT 1

Q89226
ID Q89226 standard; CDNA; 1610 BP.

AC Q89226;
DT 20-OCT-1995 (first entry)
XX
DE Human mu oploid receptor CDNA.
XX
KW Mu oploid receptor; MOR; gene therapy; diagnostic; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 239..1441
FT /tag= a
XX
PN W09507983-A.
XX
XX 23-MAR-1995.
PD
XX 13-SEP-1994; 34WO-US10358.
PE
XX 13-SEP-1993; 93US-0120601.
PR
XX (INDV) UNIV INDIANA FOUND.
PA
XX YU L;
XX
XX WPI; 1995-131351/17.
DR P-PSDB; R71966.
XX
XX New nucleic acid encoding new human mu oploid receptor - and
PT related vectors, transformed cells, antibodies etc., useful in
PT diagnosis, treatment and drug screening.
XX
XX Claim 5; Page 208-210; 266pp; English.
XX
XX A CDNA library constructed from human caudate nucleus mRNA was
CC screened with rat mu oploid receptor CDNA under conditions of
CC low stringency. One positive clone included the sequence given
CC Q89226, encoding a mu oploid receptor MOR (R71964). The CDNA
CC is used for prodn. of recombinant MOR, in gene therapy, etc.
XX
SQ Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T; 0 other;

XX	06-AUG-1998.
PD	
XX	
PF	02-FEB-1998; 98WO-DE00382.
XX	
PR	03-FEB-1997; 97DE-1003925.
XX	
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
PI	
XX	Hoehle M, Wendel B;
DR	WPT, 1998-437487/37.
XX	
PT	New genomic and cDNA sequences encoding human mu-opioid receptor -
PT	used, e.g. to predict pre-disposition to addiction and for
XX	
XX	development of analgesics, anaesthetics and anti-addiction agents
PS	
XX	Claim 8; Page 14-15; 26pp; German.
CC	
CC	This sequence encodes a novel human mu-opioid receptor. This sequence and
CC	its variants, polymorphisms and mutants are used in a method for
CC	detecting pre-disposition to disease, particularly addictive disease, by
CC	isolating DNA from a sample, genotyping selected positions and comparing
CC	with a reference DNA. Such sequences are used to develop analgesic,
CC	anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
CC	genes and vectors, particularly for pharmaceutical development, to
CC	develop diagnostic kits for predicting risk of addiction, response to
CC	analgesics or anaesthetics, or development of side effects from a drug.
CC	Particular applications are to determine risk of addiction to opiates or
CC	cocaine, or of developing inherited alcoholism.
XX	
SO	Sequence, 2162 BP/-562 A; 565 C; 458 G; 575 T; 2 other;

Query Match	Similarity	99.7%	Score 1256:	DB 19:	Length 2162:
Best Local	Similarity	99.7%	Fred. No. 0:		
Matches 1576:	Conservative	0:	Mismatches	4:	Indels 1; Gaps 1.
QY	28	TGGGAGGGGGCTATACGCGAGAGAGAAATTCAGATGCTCAGCTCGATCCGCTCCGCGCTGA	87		
Db	1	tgggagggggcctatcgcgcagagagaaatgctcagatgctcagctggtccctccgcctcga	60		
QY	88	CGCTCTCTCTGTCTCAGCCAGAGACTGGTTTCTGTAGAAGACGACGAGAGCTGTGGCAGC	147		
Db	61	cgtctctctctgtccagccagagactggttctgttaagaacagcaagsgctgtgacagc	120		
QY	148	GGCGAAAGAGAACCGGCTGAGGCGCTTGGAAACCCGAAAAGTCTCGTGCTCTCTGCTACTCT	207		
Db	121	ggcgaagaagaaacggcgtgaagcgcttggaacccgaaatctcgtgtgctccctggctacct	180		
QY	208	CGCACAGC-GTCCCGCGCGCGCGCGCTGACAGTACATGAGACGACGAGCGGTGCCCCACGAAAG	266		
Db	181	cgcacaagcgggtgtcccgccggccgctcagtaacctatggaacgaagcgctgcccccaagaa	240		
QY	267	CCAGCAATTCGACTGATGCTTGCGGCTACGTTGCTCCACAGCACCAGCACCOCGGTT	326		
Db	241	ccagaatctgcactgatgctgtggtactcaagtgtgtccccagcaaccagcccggt	300		
QY	327	CCTGGGCTAACCTGTGCCCACTTAAGTGGCAACCTGTCCGACCCATGAGGTCGGAACCGCA	386		
Db	301	cttgggttaactgtgtccacttagatgtgcaacctgtccgacccaatgctgtccgaacgcga	360		
QY	387	CGGACCTGGCGGCGGAGAGACAGCTGTGGCCCTCGGACCGGAGTGCCTTCATGATCAGCG	446		
Db	361	ccaactctggcgggagaaacagccgtgtgcccccgcgacgcgcaagctccctccatgatacagg	420		
QY	447	CCATCAGCATGCGCCCTCTACTCCATCGTGGGTGGGTCTTGGAAACTTTC	506		
Db	421	ccatcagcatatgccccttactccatcgtgtggtgtgtggtccttcgaaacttcc	480		
QY	507	TGGTCATGATGTGATTGTGCATATACACCAATGAAGCTCCGACCAACATCTACATT	566		
Db	481	tggtatcatatgtgtgtgtcagatatccaaatgaagctgtccacccaactctcatatt	540		

QY	567	TCACCTTGCTCTGGCAGATGCTCTTAGCCACCAGTACCTGCCCTCCAGAGTGTGAAT	625
Db	541	tcaccttgctcttgccagatgaccttagccaccagiatcccttgccctccagagtgtaatt	600
QY	627	ACCTAATGGGAACATGGCCATTGGAAACCATCTTTGGACGAATAGATCTCCATAGAT	688
Db	601	acctaatggaacatgaccttggcaatcttggaaacctcttggcaagatagatctccaagatt	660
QY	687	ACTATACATTTTCACGACATATTCACCCCTGACACCATGAGTGTGTGATGATCATTTG	746
Db	661	actataacatgttcacgacatatccaccctctgcacacatgagtgtgtatgcatacatgt	720
QY	747	CAGTGTGCCACCCGTGAAGGCCCTTAGATTTCGTACTCTCCCGAAATGGCAAAATTATCA	806
Db	721	cagltgtgccaccctgtgaaggcccttaagcttaccgatctcccgaaaatggcaaaattatca	780
QY	807	ATGCTGCAACTGGATCCTCTCTTTCAAGCCATTTGGTGTCTCTGTAAATGTATAGGCTACAA	866
Db	781	atgtctgaactggtatcctctctcttcagccatgtgtctctcgttaatgtatctagtccaaa	840
QY	867	CAAAATACAGCAAGGTTCCATAGATTGTACACTAACATTCTCTCATCTCAACCTGTACT	926
Db	841	caaaatacaggcaaggcttcataagattgttacaatacatctctccaccaacctgtact	900
QY	927	GGGAAGAACTCTCAAGATGCTGTTTTCATCTTCGCTTCATATATGACAGTGCATCA	986
Db	901	gggaaaacctcgtigaagaatcgtgttttcaatctctgccttcattatgcccagtgccatca	960
QY	987	TTACCGTGTCTATGACATGATGATCTTGGCCCTCAAGAGTGTCCGATGCTCTGTGCT	1046
Db	961	ttaccgtgtctatgacatgatatgattctggccctcaagagtgtccgacatgctctgtgct	1020
QY	1047	CCAAAAGAAAAGACAGGATCTTTCGAAAGATCACAGATGGTGGTGGTGGTGGGCTG	1106
Db	1021	ccaaaagaaaagacaggaaatcttcgaaagatccaccagaaagtgctgggtgggtggctg	1088
QY	1107	TGTTGATGTTGCTGGAGCTCCCATTCACATTTACGTCACTTAAAGCCTTGTTACAA	1166
Db	1081	tgttatcgctgtgtagctaccatcacattagctcaatlaaagctctgtttcaaa	1144
QY	1167	TCCCAAGAACTACCTTCCACAGCTTTCTTGGACCTTGCACTTGCTGATGCTAGTTACAA	1222
Db	1141	tcccagaaacaagcttcccaagcgttctctgcaactctgcattgctctagttacaaca	1200
QY	1227	ACAGCTGCCTCAACCCAGCTCTTTATGATTTCTGATGATAAACTCAACACATCCTTCA	1286
Db	1201	acagctgctctaaccacgctccttattgcatcttctgtatgtaaaaacttcaaaagatgcttca	1266
QY	1287	GAGAGTTCTGTATCCCAACCTCTTCCAACTTGAGCAGACAAAACCTCCACTGCAATTGCTC	1346
Db	1261	gagagttctgtatcccaacctcttccaacaatltagaacaaaactccaactcgaattctgc	1320
QY	1347	AGAACTACAGAGACCCACCCCTCCACGGCCCAATACAGTGTATGAACTAATCATCTAGCTAG	1406
Db	1321	agaaactacagagaccaccttccaagggccaatcacgtatgtgaactaatcatcagcttag	1380
QY	1407	AAAATCTGGAAGCAGAACTGCTCCGTTGGCCTTACAGGGGTCTCATGTCATCCGACCTT	1466
Db	1381	aaaatctggaagcagaactgctccgttgccttaacagtgctcatgcccattccgaactt	1440
QY	1467	CACCAAGCTTAGAGCCACCATATGATGTGGAACAGAGTGTGCTTCAAGAAATGTGTAGAGG	1526
Db	1441	caccaagcttagaagccacacatgatagttgaaacagtgctctcaagaaatgtgtagagag	1500
QY	1527	CTCTAATATCTTATAGAAAGTCCGTGCTTTTAGTGTCACTCCAACTCTTTCTCTTGAGCA	1588
Db	1501	ctctaatctcttaggaagagtcctactttagtgatccaacacctcttcctctctgscac	1566
QY	1587	CTCTGCTCTGACATTTAGAGG 1607	
Db	1561	ctctgctctgacatttagagg 1581	

RESULT	3
ID	V61995
AC	V61995 standard; cDNA; 2162 BP.
XX	
XX	V61995;
XX	
DT	11-JAN-1999 (first entry)
XX	
DE	Human mu-opioid receptor cDNA variant 11.
XX	
KW	Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW	predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KW	psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KW	cocaine; inherited alcoholism; human; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	CDS
FT	213..2040
FT	/*tag- a
FT	/product- "mu-opioid receptor"
FT	502..503
FT	/*tag- b
FT	/note- "Site of Intron 1"
FT	855..856
FT	/*tag- c
FT	/note- "Site of Intron 2"
FT	1376..1377
FT	/*tag- d
FT	/note- "Site of Intron 3"
FT	1613
FT	/*tag- e
FT	/note- "Wild type G is replaced by C"
XX	
PN	W09833937-A2.
XX	
PD	06-AUG-1998.
XX	
XX	
PE	02-FEB-1998; 98MO-DE00382.
XX	
PR	03-FEB-1997; 97DE-1003925.
XX	
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
PI	
PI	Hoehe M, Wendel B;
DR	WPI; 1998-437487/37.
XX	
XX	
PT	New genomic and cDNA sequences encoding human mu-opioid receptor -
PT	used, e.g. to predict pre-disposition to addiction and for
PT	development of analgesics, anaesthetics and anti-addiction agents
XX	
SS	Claim 8; Page -: 26pp; German.
XX	
XX	
CC	This sequence encodes a novel human mu-opioid receptor in which a G
CC	nucleotide at position 1613 of the wild-type sequence represented in
CC	V61994 is replaced by a C. The wild type receptor and its variants,
CC	polymorphisms and mutants are used in a method for detecting
CC	predisposition to disease, particularly addictive disease, by isolating
CC	DNA from a sample, genotyping selected positions and comparing with a
CC	reference DNA. Such sequences are used to develop analgesic, anaesthetic,
CC	anti-addictive and psychopharmaceutical agents; to construct genes and
CC	vectors, particularly for pharmaceutical development, to develop
CC	diagnostic kits for predicting risk of addiction, response to analgesics
CC	or anaesthetics, or development of side effects from a drug. Particular
CC	applications are to determine risk of addiction to opiates or cocaine, or
CC	of developing inherited alcoholism.
CC	Note: This sequence is not represented in the specification and has
CC	been constructed from the wild-type sequence represented in V61984 in
CC	accordance with the specification.
XX	

Query Match	78.0%	Score 1256;	DB 19;	Length 2162;
Best Local Similarity	99.7%	Pred. No. 0;		
Matches 1576;	Conservative	0;	Mismatches 4;	Indels 1;
				Gaps 1;
QY 28 TGGGGGGGGCTTATACCGAGAGAGAGATGTCAGATGTCACGTGGCTCCCGCCCTGA 87				
Db 1 tgggaggggggtacacagagagagagagatgtagatgctccagctggtccctccgcctga 60				
QY 88 CGCTCTCTCTCTGTCTCAGCCAGACGTGGTTCTGTATAGAAACAGCAGAGAGCTGTGGACG 147				
Db 61 cgtctctctctgtctcagccagagactggtttctgtaagaacaagagagactgtgtgacgc 120				
QY 148 GGCGAAAGAGCGGCTGTAGGCGCTTGGAAACCCGAAAGTCTCGTGTCTCGGTACT 207				
Db 121 ggcgaagaagagcgcgctgagcgcttggaaacccgaaagctctggtgtctcgtgctacc 180				
QY 208 CGCACAGC -GTGCCCGCGCGCGCTCACTTACATGAGACAGAGCGCTCCCGCAGAAAG 266				
Db 181 cgcacagagcggtccgcgcgcgcgtcagtagacatgagagagagcgctgcccccaagacg 240				
QY 267 CCAGCAATTCGACACTGATGCTCTTGGCGTACTGAAGTCTCTCCAGCACACCAGCCGGTT 326				
Db 241 ccaagaattgcacgtatgctcttggcgttctaagttgtctcccaagacaccagccccggt 300				
QY 327 CCTGGGTCAACTTGTGCCCACTTAGATGGCAACGTCGCGACCCGATCGGTCGGAACGCA 386				
Db 301 ccgtgggtcaactgttcccaacttagatggcaaccggtccgcacccatggtgtccgaacgca 360				
QY 387 CCGACCTGGCGGGAGAGACAGCCTGTGCGCTCCGACCGGAGTGCTCCATGATCAGG 446				
Db 361 ccaacctgggggagagagacagcctgtgcctccgcagccgacgtccctccatgatacag 420				
QY 447 CCATCAGCATATGAGCCCTTACTCCATCGATCGTGCGTGGGGTCTTCGAAACTTCC 506				
Db 421 ccatcacaatcattagccctccatccacatcggtgcggtgggggtcttcggaacttcc 480				
QY 507 TGTGATATATGATATTGTACGATACACCAAGATGAAAGACTGCCACCAACATCTACATTT 566				
Db 481 tgttcattatgattgattgttcagatatacacaagaatgaaagactgcacacaatctacatt 540				
QY 567 TCAACCTTGGCTCTGGCAGATGCCTTTAGCCACACAGTACCCTTGGCCTTCCAGAGTGGATT 626				
Db 541 tcaacctgtctctggtcagatgctcttagcacaacagatccctccctccaagatgtygaatt 600				
QY 627 ACCTAATGGGAACATGGGCATTTGGAACATCTTTGCAAGATAGTATCTTCATAGATT 686				
Db 601 acctaatgggaactgtgcatcttggaaacacatccttgaagaatagtgtctcccatagatt 660				
QY 687 ACTATACATGTTACACGACATATTACCCCTTGACCATGATGAGTGTGATGATACATTG 746				
Db 661 actataaatgttcaaccgcgcatctaccaccttcacacatgagtgtgatcgatbcatgt 720				
QY 747 CAGTGTGGCAACCGTGAAGGCTTAGATTTCGATTCGCCGAATCCGAAATATCA 806				
Db 721 cagtgctgcaccccgctcgaagcgcttagatttcggaaccccgaaatgycacaatatca 780				
QY 807 ATGTCTGGAACTGGATCTCTCTCTTCAGGCATTTGGTCTCTGTATGTTTCATGGCTACAA 866				
Db 781 atgtctgcaactgtagtctctcttcacgcatgtgtcttcctgtaattgtcatgctacaa 840				
QY 867 CAAATATACGACGAAGTTTCCATAGATTGTACACTTACATTTCTCTCATCCAACTGGTACT 926				
Db 841 caaaatcacaggaaggttccatagatgtatcacaaacatctctcatatccaactgtgtact 900				
QY 927 GGGAAACCTCTGTAAGTCTGTGTTTTCATCTTCGCTTATATGACAGTGGCTACCA 986				
Db 901 gggaaaaacctgtgaagatctgtgttttcaactctcgctccatcatatgcaggtctcaica 960				
QY 987 TTACCGTGTGCTATGAGATGATCTTGGCGCTCAAGATGTCCGATGCTCTCTGGCT 1046				

Db	961	ttaccgtgtcctatgtgaactgatactcttgcgctcaagaagtgtccgcatgctctctgct	1020
QY	1047	CCAAAGAAAAGGACAGAAATCTTTGGAAGATCACCAGATGGTGGTGGTGGTGGTGC	1106
Db	1021	ccaaagaaaagacagaaactcttcgaaagatcacagaga19gtgctg19gtg19gtg	1080
QY	1107	TGTTTCATCGTCTGCTGAGACTCCCATTCACATTTAGCTATCATTTAAAGCTTGGTTACA	1166
Db	1081	tgtcatcgtctcgtgcagctcccatcaatlaagtlcatlaagtaaaccttgcgttaca	1140
QY	1167	TCCCGAAGAACTAGATTCCAGACAGTGTCTTGGCACTTCGATTCATGCTCTAGGTTACACA	1226
Db	1141	tcccaagaactaagttccagacctcttcgtgaactctgcagcttgcgtctaggttaacaa	1200
QY	1227	ACAGCTGCTCTCAACCCAGTCTTTATGCAATTTCTGATGATAAAACTTCAACAGATGCTTCA	1286
Db	1201	acaagctccccaacccaagctcttla19cat1tctg19at19aaacttcaaacgatlcttca	1260
QY	1287	GAGAGTCTGTATGCCAACCTCTTCCACATGAGCAACAAATCCACTCGAATTCGTC	1346
Db	1261	gagagttctgtatcccaacctcttccaacat19agacaacaaacctccac19aat19ctc	1320
QY	1347	AGAACACTAGAGACCAACCCCTCCAGCGCCAAATACAGTGGATGAACTAATCATCAGCTAG	1406
Db	1321	agaagactagagacacacctccacg19caatag19atagaaactaatcatcaagctag	1380
QY	1407	AAAAATCTGGAAGCAGAAATCGTCTCGCTTGCCCTTACAGAGGTTCTATGCCATTCCGACTT	1466
Db	1381	aaaacttc19aagaagaagaactgtc19ct19ccctaaacag19tctcat19ccat19ccgacct	1440
QY	1467	CACCAAGCTTAGAAGCCACCATGTATGTGGAAGCAGAGTGTCTTCAAGATGTAGAGAG	1526
Db	1441	caccaagccttagaagaagccacat19tat19tgaagaacag19tgcctcaagaat19t19tagaag	1500
QY	1527	CTCTAATTCCTTAGAGAAAGTGCTGCTTTTAGTCAATCCAACTCTTTCTCTCTGCGCA	1586
Db	1501	ctcctaattcctagaagaag19cctactctt19tga19tcatcccaacctcttctctct19gcca	1560
QY	1587	CTCTGCTCTGACATTGAGG 1607	
Db	1561	ctctgctctgacatcatagaag 1581	
RESULT 4			
Q93102	ID	Q93102 standard; cDNA; 2160 BP.	
XX			
AC	Q93102;		
XX			
XX	11-DEC-1995 (first entry)		
DT			
XX	Human mu opiate receptor cDNA.		
DE			
XX	Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;		
KW	drug abuse; analgesic; ds.		
KW			
XX	Homo sapiens.		
OS			
XX			
XX	Key	Location/Qualifiers	
FT	CDS	213..1415	
FT		/*tag- a	
XX			
PN	W09520667-A1.		
XX			
PD	03-AUG-1995.		
XX			
PF	30-JAN-1995; 95MO-US01144.		
XX			
PR	28-JAN-1994; 94US-0188275.		
XX			
XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.		
PA	(USSH) US SEC DEPT HEALTH.		
XX			

PI Johnson PS, Persico AM, Uhl G, Wang J;
 XX
 DR WPI: 1995-275452/36.
 DR P-PSDB; R/6780.
 XX
 PT New DNA encoding human mu opiate receptor - used esp. for screening
 PT cpds. for activity as opiate agonists or antagonists
 XX
 PS Claim 4; Page 24-25; 49pp; English.
 XX
 CC hMOR cDNA was obt'd. from a human cerebral cortical cDNA library
 CC screened with fragments of a rat mu opiate receptor. Cloned hMOR
 CC DNA can be used as probes to examine the structure and function of
 CC hMOR genes or to screen individuals for susceptibility to drug
 CC abuse. Expression in e.g. COS cells allows production of
 CC recombinant hMOR.
 XX
 XQ Sequence 2160 BP; 563 A; 566 C; 455 G; 576 T; 0 other;

Query Match	77.0%;	Score 1240;	DB 16;	Length 2160;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 1560;	Conservative 0;	Mismatches 4;	Indels 1;	Gaps 1;
QY 44	GAAGAGGAGATGTCAGATGCTCAGCTGGGTCCTCCGCTCGCTGAAGGCTCTGTGCTC	103		
Db 17	gcagagggagatgtagcagctcagctcgtgtccctccgctgaagccctctgtctc	76		
QY 104	AGCCAGACTGATTCTCTAAGAAAACAGCAGAGCTGTGGACGGCGGAAAAGGAGCGC	163		
Db 77	agccagagctgtgtctctgtaagaaacagcagagctgtgtgagcggcggaaggaagcgcc	136		
QY 164	TGAGGCGCTTGGAACCCGAAAAGTCTGGGTCTCTGGCTACTCTGCACAC - GTGCCG	222		
Db 137	tgaagcgctgtgaaccgcaaaagttcgtgtcctgtctacccctgcacaagcgggtgccg	196		
QY 223	CCGGCCCTCATGTACATGAGCAGAGGGCTGCCGCCACGAGCGCACCATTTGCATGA	282		
Db 197	ccggccgctcgttacatgagacagagcgctgtcccccagcaagccgaatgtcactga	256		
QY 283	TGCCTTGGCGTACTCAAGTTGCTCCCGACACAGCCCGGGTTCTTGGGTCAACTGTC	342		
Db 257	tgcccttgcgtactaagttgtctccagcaaccagcccggttctcgttcaactgtc	315		
QY 343	CCACTTAATSGCAACCTGTCCGACCCATGGGGTCCGAACCGCACCGACTGGCGGAG	402		
Db 317	ccacttaagtgtgcaacctgttcgcagccctcgtgtccagccagcccaacctgggcggag	376		
QY 403	AGACAGCCTGTGGCCTCGCAGCGGAGTCCCTCATGTATCAAGGCGATCAGATATGC	462		
Db 377	agacagcctgtgcccctccagccggagccctccatgtatcagcgacacacagatcaagc	436		
QY 463	CCTTACTCATCGTGTGCGGTGTGGGGCTTTGGAAACTCTCGTATGATGTAT	522		
Db 437	ccttactcatcgt	406		
QY 523	TGTCAATACACCAAGATGAAGACTGCCACCAACATCTACATTTTCAACTTGGCTTGC	582		
Db 497	tgctcagatataccaagatgaagactgtccacaacatctacatlttcaacctgtgtcgtgc	556		
QY 583	AGATGCCCTTACCAACCATATCCCTGGCCTTCAGAGTGTGAATTAACCTAATGGGAATG	642		
Db 557	agatgccctttagccacagctacccgtgcccctccagagtgtaattcaacctaaagggaaatg	616		
QY 643	GCCATTTGGAACCATCTTTTGCAGATAGTATCTCCATTAATTACTTAAATCATGTTAC	702		
Db 617	gccatttgaaccatccttgcagatagtgtatctccatagattactataacatggttcac	676		
QY 703	CAGCATATTCAACCTCTGTACCATATGATGTGTGATCGATACATTGCACTGTCCACCTGT	762		
Db 677	cagcatattccacctgtcaccaatgaagtggtgtatcgtatacatctgcagagctgtccacctgt	736		
QY 753	CAGGCGCTTAATTTCCGTACTCCCGGAAAAGCCAAAATTTCATGTCGTCTCACTGGAT	822		

```

Db 737 caagcccttagatcttcgactcccccgaatgccaataatcatgctcgaactgat 796
QY 823 CCTCTCTACCCAGCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 882
Db 797 cctctctcagccatctgctcctcctgtaatgcttcaagaaataacagcaagg 856
QY 883 TTCCATAGATGTAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 942
Db 857 ttccatagatgtaacatctcctcctgtaatgcttcaagaaataacagcaagg 916
QY 943 GATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1002
Db 917 gatctgtctctctctctctctctctctctctctctctctctctctctctctct 976
QY 1003 ACTGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1062
Db 977 actgatgactctgcccctcaagagctcctctctctctctctctctctctctct 1036
QY 1063 GAATCTTGAAGGATCACCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1122
Db 1037 gaatcttgaagatcaccagagatgctgctgctgctgctgctgctgctgctgctg 1096
QY 1123 GACTCCCATTCACATTTACGTCATTAAGCCCTGTTACATCCAGAAATAGCTT 1182
Db 1097 gactcccatcacaattacatcattcaagccttggttacaacccagaactagct 1156
QY 1183 CCACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1242
Db 1157 ccaagactctctctgacctctgactgctcaggttacaacaaagctcctcaacc 1216
QY 1243 AGTCTTTATGCAATTTCTGATGAAGAACTTCAACGATGCTTCAAGAGTTCTGATCC 1302
Db 1217 agtctttatgcatcttgatgtaaaacttcaaaagctcagaggttctgctatccc 1276
QY 1303 AACCTTTCCAAATTTGAGCAACAACAACTCCACTGGAATGCTGGAACACTAGACCA 1362
Db 1277 aacctcttccaaacttgagcaacaactccactgcaatcgtcagaaacactagagacca 1336
QY 1363 CCCGCCGCGGCAATAGAGATGAGAACTAATCATCAGCTAGAGAAATCTGGAAGACA 1422
Db 1337 ccccccgcgcgaataaagtggaagaacaaatcaatcagtagaagaactctggaagcga 1396
QY 1423 AACTGCTCGTGGCCCTTAACAGGGGTCTCATGCGAATCCGACTTCCAGAGTTAGAAC 1482
Db 1397 aactgctcgttgcccttaacaggggtctcatgctcagacttccaaagcttagaagc 1456
QY 1483 CACCATGATGTGGAAGAGAGTTGCTTCAAGAAATGTAAGAGGCTTAATTTCTAGGA 1542
Db 1457 caccatgatactggaagagaggttgcttcaagaatgtaggaagagctcaattctcaga 1516
QY 1543 AAGTCCGCTGTTTATGAGCATCAACACTCTTCTCTCTGAGCACTGCTCTGACACT 1602
Db 1517 aagtgccactcttagtcaatccaaacctcttccctctgagcactctgctcagact 1576
QY 1603 AGAGG 1607
Db 1577 agagg 1581

```

```

RESULT 5
ID 288470
ID 288470 standard; DNA; 2162 BP.
AC 288470;
XX
XX 11-MAY-2000 (first entry)
XX
XX Human mu opioid receptor gene.
XX
XX Human mu opioid receptor: hMOR1; diagnosis: addiction; constipation;
XX diarrhoea; decreased immune response; stress; gastrointestinal motility;
XX immune response; hypothalamus pituitary adrenal axis; gonadal axis.

```

```

KW pain; opioid; cocaine; nicotine; barbiturate; sedative hypnotic;
KW anxiolytic; alcohol; ds.
XX
OS Homo sapiens.
PN MO200003024-A2.
XX
XX 20-JAN-2000.
XX
XX 10-JUL-1999; 99MO-US15707.
XX
XX 10-JUL-1998; 98US-0113426.
XX
XX 09-JUL-1999; 99US-0113426.
XX
PA (UYRO.) UNIV. ROCKEFELLER.
PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX
XX Kreek MJ, LaForge KS, Yu L, Tischfield JA;
XX
XX WPI; 2000-160930/14.
XX
XX P-PSDB; Y79945.
XX
XX New human opioid mu receptor gene variant for determining
XX susceptibility of a subject to addictive disorder, pain -
XX
XX Claim 1; Page -; 134pp; English.
XX
CC The present invention describes an isolated variant (V) of the human
CC mu opioid receptor (hMOR1) gene with at least two variations A118G,
CC C117, G24A, G775A or G942A of the sequence of Genbank accession number
CC L25119. Determination of increased or decreased susceptibility in a
CC subject to at least one addictive disorder like opioid, cocaine,
CC nicotine, barbiturate or sedative hypnotic, anxiolytic, alcohol
CC addiction or addiction to others psychostimulants and to pain is done
CC by determining the presence of (V) with variation A118G or C117T
CC respectively in one and/or both alleles of (V) and it can also be done
CC by determining the presence of the hMOR1 protein with variation Asn40Asp
CC or Ala6Val respectively. Therapeutically effective amount of pain
CC reliever to induce analgesia or therapeutic agent to treat one additive
CC disorder is determined by determining the variations in the hMOR1 gene
CC or protein and so increased or decreased susceptibility indicates an
CC increased or decreased amount of pain reliever or therapeutic agent
CC respectively. The determination of the hMOR1 gene with variation A118G
CC or C117T also helps in the diagnosis of a disease or disorder like
CC infertility, constipation, diarrhoea, decreased immune response or
CC decreased ability to withstand stress related to physiological function
CC like sexual or reproductive function, gastrointestinal motility, immune
CC response, or ability to withstand stress regulated by hypothalamus
CC pituitary adrenal axis (HPA) or gonadal axis (HPG). The present sequence
CC represents the hMOR1 gene.
CC N.B. The present sequence is not given in the present invention but
CC is referred to as the Genbank accession number L25119.
XX
XX Sequence 2162 BP; 563 A; 566 C; 455 G; 576 T; 2 other;

```

```

Query Match 77.0%; Score 1240; DB 21; Length 2162;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1560; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

```

Accession	Gene	Species	Chromosome	Start (bp)	End (bp)	Strand	Length (bp)	GC Content (%)	Exons	Introns	Annotations
U01101	mu-opioid receptor	Human	12	11,199,000	11,199,100	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01102	mu-opioid receptor	Human	12	11,199,100	11,199,200	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01103	mu-opioid receptor	Human	12	11,199,200	11,199,300	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01104	mu-opioid receptor	Human	12	11,199,300	11,199,400	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01105	mu-opioid receptor	Human	12	11,199,400	11,199,500	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01106	mu-opioid receptor	Human	12	11,199,500	11,199,600	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01107	mu-opioid receptor	Human	12	11,199,600	11,199,700	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01108	mu-opioid receptor	Human	12	11,199,700	11,199,800	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01109	mu-opioid receptor	Human	12	11,199,800	11,199,900	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01110	mu-opioid receptor	Human	12	11,199,900	11,200,000	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01111	mu-opioid receptor	Human	12	11,200,000	11,200,100	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01112	mu-opioid receptor	Human	12	11,200,100	11,200,200	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01113	mu-opioid receptor	Human	12	11,200,200	11,200,300	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01114	mu-opioid receptor	Human	12	11,200,300	11,200,400	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01115	mu-opioid receptor	Human	12	11,200,400	11,200,500	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01116	mu-opioid receptor	Human	12	11,200,500	11,200,600	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01117	mu-opioid receptor	Human	12	11,200,600	11,200,700	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01118	mu-opioid receptor	Human	12	11,200,700	11,200,800	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01119	mu-opioid receptor	Human	12	11,200,800	11,200,900	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01120	mu-opioid receptor	Human	12	11,200,900	11,201,000	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01121	mu-opioid receptor	Human	12	11,201,000	11,201,100	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01122	mu-opioid receptor	Human	12	11,201,100	11,201,200	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01123	mu-opioid receptor	Human	12	11,201,200	11,201,300	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01124	mu-opioid receptor	Human	12	11,201,300	11,201,400	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01125	mu-opioid receptor	Human	12	11,201,400	11,201,500	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01126	mu-opioid receptor	Human	12	11,201,500	11,201,600	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01127	mu-opioid receptor	Human	12	11,201,600	11,201,700	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01128	mu-opioid receptor	Human	12	11,201,700	11,201,800	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01129	mu-opioid receptor	Human	12	11,201,800	11,201,900	+	101	41.6	1	0	Human mu-opioid receptor cDNA variant 1.
U01130	mu-opioid receptor	Human	12	11,201,900	11,202,000	+	101	41.6	1	0	Human mu-opioid

OY 1227 ACAGCTGCTCAACCCAGCTCTTATGATTTCTGGATGAAAACCTCAACGATGCTTCA 1286
 DB 1201 AACGCTGCTCAACCCAGCTCTTATGATTTCTGGATGAAAACCTCAACGATGCTTCA 1260
 OY 1287 GAGAGTCTGTATCCCACTCTTCAACATTTAGACCAACAAATCTCACTCGAATTCGTC 1346
 DB 1261 GAGAGTCTGTATCCCACTCTTCAACATTTAGACCAACAAATCTCACTCGAATTCGTC 1320
 OY 1347 AGACACTAGAGACACCCCTTCACGCGCCAAATACAGTGTAAATCAATCAATCACTAG 1406
 DB 1321 AGAACACTAGAGACACCCCTTCACGCGCCAAATACAGTGTAAATCAATCAATCACTAG 1380
 OY 1407 AAAATCTGGAACCAAGAACTGCTCGTGGCTTACAGAGGCTTCATGGCATTCGACACTT 1466
 DB 1381 AAAATCTGGAACCAAGAACTGCTCGTGGCTTACAGAGGCTTCATGGCATTCGACACTT 1440
 OY 1467 CACCAAGCTTAGAGACCAACCAATGTATGTGAAGCAGTGTCTTCAAGATGTGTAGAGG 1526
 DB 1441 CACCAAGCTTAGAGACCAACCAATGTATGTGAAGCAGTGTCTTCAAGATGTGTAGAGG 1500
 OY 1527 CTCTAATTTCTAGAGAAAGTCTGCTTTAGGTCATCCAACTCTTCTCTGCGCA 1586
 DB 1501 CTCTAATTTCTAGAGAAAGTCTGCTTTAGGTCATCCAACTCTTCTCTGCGCA 1560
 OY 1587 CTCTGCTGACATTAAGG 1607
 DB 1561 CTCTGCTGACATTAAGG 1581

RESULT 8
 V61987
 ID V61987 standard; cDNA; 2162 BP.
 AC V61987;

DT 11-JAN-1999 (first entry)
 XX Human mu-opioid receptor cDNA variant 3.

XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 KW predilection; addiction; analgesic; anesthetic; anti-addictive;
 KW psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
 KW cocaine; inherited alcoholism; human; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX

XX Key Location/Qualifiers
 FT CDS 213..2040
 FT /*tag- a
 FT /product- "mu-opioid receptor"
 FT 502..503
 FT /*tag- b
 FT /note- "Site of intron 1"
 FT 855..856
 FT misc_feature
 FT /*tag- c
 FT /note- "Site of intron 2"
 FT 1376..1377
 FT /*tag- d
 FT /note- "Site of intron 3"
 FT 102
 FT mutation
 FT /*tag- e
 FT /note- "Wild type C is replaced by T"

XX W09833937-A2.
 PN 06-AUG-1998.
 XX 02-FEB-1998; 98WO-DE00382.
 XX 03-FEB-1997; 97DE-1003925.
 PR

PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

XX Hoehe M, Wendel B;

XX WPI; 1998-437487/37.

PT New genomic and cDNA sequences encoding human mu-opioid receptor -
 PT used, e.g. to predict pre-disposition to addiction and for
 PT development of analgesics, anaesthetics and anti-addiction agents
 XX
 PS Claim 8; Page -; 26pp; German.

CC This sequence encodes a novel human mu-opioid receptor in which a C
 CC nucleotide at position 102 of the wild-type sequence represented in
 CC V61984 is replaced by a T. The wild type receptor and its variants,
 CC polymorphisms and mutants are used in a method for detecting
 CC predilection to disease, particularly addictive disease, by isolating
 CC DNA from a sample, genotyping selected positions and comparing with a
 CC reference DNA. Such sequences are used to develop analgesic, anesthetic,
 CC anti-addictive and psychopharmaceutical agents, to construct genes and
 CC vectors, particularly for pharmaceutical development, to develop
 CC diagnostic kits for predicting risk of addiction, response to analgesics
 CC or anaesthetics, or development of side effects from a drug. Particular
 CC applications are to determine risk of addiction to opiates or cocaine, or
 CC of developing inherited alcoholism.
 CC Note: This sequence is not represented in the specification and has
 CC been constructed from the wild-type sequence represented in V61984 in
 CC accordance with the specification.
 XX

S0 Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 2 other;

Query Match 74.8%; Score 1205; DB 19; Length 2162;

Best Local Similarity 99.6%; Pred. No. 0; Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

OY 28 TGGAGAGGGGCTATACGACGAGAGAAATGCATGCTACCTGCTCCGCTGA 87
 DB 1 tggagagggggtatacgaagagagagatgtcagctgcagctgcgcctcga 60
 OY 88 CGCTCTCTCTGTCTACGACGAGACTGTTTCTTAAGAAACACAGAGCTGTGGCAGC 147
 DB 61 cgcctcctctcgtctcagccagagactgttctctlaagaaatagcagagctgtgagc 120
 OY 148 GGGGAAAGGAAGCGGCTGAGGCGCTTGGAAACCCAAAAGTGTGCTGCTGCTACT 207
 DB 121 ggcgaagaaagcgctgagcgcttgaacccgaaagcttgcgtctcctgtactact 180
 OY 208 GCGACAGC-GTGGCCGCGCCGCGCTCAGTACATGACAGCAGCGCTGCCCGACGAGC 266
 DB 181 gcacagcggtgccccgcgcgcgtacagtagcagagagcgctgcgcccaagacg 240
 OY 267 CCAGCAATGACATGATGCTTGGCGTACTAATTTGCTCCCGACAGACGCGCGGTT 326
 DB 241 ccagcaatgacatgactgcttgcgtactcaagttgtcccccagacccgcgcggt 300
 OY 327 CCTGGGTCAACTTGCCCACTTAAATGGCAACCTGTCCGACCACTGGCGGTCCGACGCA 386
 DB 301 cctgggtcaacttgcctcaacttaagtagcaacccgtccagaccatggtgtcgaacgca 360
 OY 387 CCGACCTGGGGGAGAGACAGCGCTGTGCCCTCCGACCGGAGTCCCTCATGATCAGG 446
 DB 361 ccaacctgggggagagagacagcctgtgcctccgacccgagcctccatgtatcagc 420
 OY 447 CCATCAGATATGAGCCCTCTACTCATCGTGTGCTGTGGGGCTCTTGGAAATCTCC 506
 DB 421 ccatacagatcatgagcctcctaccatcagctgtgctgtgtgtgtgtgtgtgtgtgt 480
 OY 507 TGGTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 566
 DB 481 tggatcatgatatgatatgatatgatatgatatgatatgatatgatatgatatgatat 540
 OY 567 TCAACCTTGCTCTGGCAGATGCTTAGCACAACAGTACCTGCTTCCAGAGTGTGAT 625

```

Db 541 tcaacctgtcttcgcaatgctcttagccacacagtaacctgtccctccagatgagtaatt 600
Oy 627 ACCTATATGGAAACATGCGCATTGTGGAACCATCTTGGCAAGATAGTATCTCCATAGATT 686
Db 601 acctaatggaacatagcatttggaaccatctcttgcaagatagatgattccatagatt 660
Oy 687 ACTATAACATGTTCCACGACATATCACCCCTCTGCACCATGATGATGTTGATCATCATTTG 746
Db 661 actataaacatgtccacgacatattacacctctgcacatgagatgltgtatgatacatg 720
Oy 747 CAGTGTCCACCCCTTCAAGGCTTAGATTTCGTTACTCCCGAAATGCCAAATATTATCA 806
Db 721 cagttctgcacaccttgcaagccttagatttccgtactcccccgaatagcacaatatca 780
Oy 807 ATGTCTGCACTGATCCTCTCTTCCAGCCATTGGTCTTCTGTAATGTTATGATGCTACAA 866
Db 781 atgtctgcaactgatactctctcttcagcaattgtcttcctgtaattgtatgctgacaa 840
Oy 867 CAAATATACGCAAGGTTCCATAGATTGTACACTAATCTCTCATCTCCAACTGGTACT 926
Db 841 caaatataaggaaggttccatagatgtacacatacattctccatcccaacctgtaact 900
Oy 927 GGGAAACCTGCTGGAAGATCTGTGTTTCATCTTGCCTTCAATTAGCCAGTGCATCA 986
Db 901 gggaaacctcgtagaagatctgttctcatcttcgcttcatatgccaagtccatca 960
Oy 987 TTACCGTGTCTANGAGTATGATCTTGGCGCTCAAGAGTCCGCATGCTCTGTGCT 1046
Db 961 ttaccgtgtctatgactgatacttctgacctcaagaggtgtccgcatgctctctgct 1020
Oy 1047 CCAAGAAAGAGACAGATCTTTCAGAGATACACAGATGCTGTGGTGGTGGCTG 1106
Db 1021 ccaaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 1080
Oy 1107 TGTTCATGCTGCTGCTGACTCCCATTCATTTAGCTCATCTTAAGGCTTGGTTACAA 1166
Db 1081 tgttcactgctcgtcgtgactcccatcaatttaagctatcaatgaagccttggttaaca 1140
Oy 1167 TCCAGAAACTAGCTTCCAGACTGTTTCTGGCACTTGCATCTGCTCTAGTTACACA 1226
Db 1141 tccagaaactagcttccagactgttcttgcacttctgcattgtctaggtttacaca 1200
Oy 1227 ACAGTGTGCTCAGCCAGCTCTTATGATTTCTGATGAATAAATCAACGATCTTCA 1286
Db 1201 acagctgtcctcaacccaaagcttcaatgcaattcgtgaataaactcaacagatgttca 1260
Oy 1287 GAGAGTCTGTATCCCAACCTCTTCCAACTAGGACAAACAACTCCATCATTTGCTC 1346
Db 1261 gagaattctgtatcccaactcttccaaacttgagcaacaacaaactccactgaaattgttc 1320
Oy 1347 AGAACACTAGAGACACCCCTTCCAGGCCAATATAGTGTAGAACTAATCATCAGCTAG 1406
Db 1321 agaacaactagagaacacccctccacagcccaatacagtagtaagaaataatcatcagctag 1380
Oy 1407 AAAATCTGGAAGCAAAACTGCTCCGTTGCCCTAACAGGGTTCATGCTATCCGACTT 1466
Db 1381 aaaatctggaagcaaaactgctccgttgccttaacaggttctcatgcatctccgacctt 1440
Oy 1467 CACCAAGCTTAAAGCACCACATGATGTGGAAGAGTGTCTTCAAGAAATGTGTAGAGG 1526
Db 1441 caccaagcttgaagacacacatgatagtggaagcaggtgtgtcctaagaatgtgtgaggg 1500
Oy 1527 CTCTAATCTCTAGGAAAGTGCCTCTTTAGGTATCCAACTCTTTCTCTCTGCGCA 1586
Db 1501 ctctaatctctcagaagagtgctcactttagtcatccaactcttctctctctgagcca 1560
Oy 1587 CTCTGCTCTGCACATAGAGG 1607
Db 1561 cctgtctctgcacattagagg 1581

```

RESULT 9

```

V61988
ID V61988 standard; cDNA; 2162 BP.
XX AC
XX V61988;
XX 11-JAN-1999 (first entry)
XX DE
XX Human mu-opioid receptor cDNA variant 4.
XX DE
XX Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
XX prediagnosis; addition; analgesic; anaesthetic; anti-addictive;
XX psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
XX cocaine; inherited alcoholism; human; ss.
OS Homo sapiens.
OS Synthetic.
XX Key
XX CDS
XX Location/Qualifiers
XX 213..2040
XX /tag= a
XX /product= "mu-opioid receptor"
XX 502..503
XX /tag= b
XX /note= "Site of intron 1"
XX 855..856
XX /tag= c
XX /note= "Site of intron 2"
XX 1376..1377
XX /tag= d
XX /note= "Site of intron 3"
XX 175
XX mutation
XX /tag= e
XX /note= "Wild type C is replaced by A"
XX FT
XX PN
XX WO9833937-A2.
XX 06-AUG-1998.
XX PD
XX 02-FEB-1998; 98WO-DE00382.
XX PF
XX 03-FEB-1997; 97DE-1003925.
XX PR
XX (DELB-) DELBROECK CENT MOLEKULARE MEDIZIN MAX.
XX PI Hoehe M, Wende J B;
XX DR WPI; 1998-437487/37.
XX DX
XX New genomic and cDNA sequences encoding human mu-opioid receptor -
XX used, e.g. to predict pre-disposition to addiction and for
XX development of analgesics, anaesthetics and anti-addiction agents
XX PT
XX Claim 8; Page -: 26pp; German.
XX PS
XX This sequence encodes a novel human mu-opioid receptor in which a C
XX nucleotide at position 175 of the wild-type sequence represented in
XX V61984 is replaced by an A. The wild type receptor and its variants,
XX polymorphisms and mutants are used in a method for detecting
XX prediagnosis to disease, particularly additive disease, by isolating
XX cDNA from a sample, genotyping selected positions and comparing with a
XX reference DNA. Such sequences are used to develop analgesic, anaesthetic,
XX anti-addictive and psychopharmaceutical agents, to construct genes and
XX vectors, particularly for pharmaceutical development, to develop
XX diagnostic kits for predicting risk of addiction, response to analgesics
XX or anaesthetics, or development of side effects from a drug. Particular
XX applications are to determine risk of addiction to opiates or cocaine, or
XX of developing inherited alcoholism.
XX Note: This sequence is not represented in the specification and has
XX been constructed from the wild-type sequence represented in V61984 in
XX accordance with the specification.
XX CC
XX Sequence 2162 BP; 563 A; 564 C; 458 G; 575 T; 2 other:

```

Query Match 74.8%; Score 1205; DB 19; Length 2162;
 Best Local Similarity 99.6%; Pred. No. 0; Mismatches 5; Indels 1; Gaps 1;
 Matches 1573; Conservative 0;

28 TGGAGGGGGCTATACGAGAGAGAGATGTCAAGTCTCAGTCCGTCCTCCCTCGA 87
 1 tggaggggggctatacgagagagagatgtcagtcagtcagtcgctccctcgctga 60
 88 CGCTCTCTCTGTCTCAGCAGAGAGTGTCTGTGAAGAAAGAGAGAGTGTGAGC 147
 61 cgtctctctgtctcagcagagagagctgttctgtlaagaaagagagagctgtgca 120
 148 GGGGAAAGAGAGGGCTGAGGGCTTGGAAAGCCGAAAGTCTGGGGCTCCGGTACT 207
 121 ggggaaagagagggctgagggcttggaaagccgaaagctccggctgctcgtaacct 180
 208 GGCACAGC-GTGCCCGCCCGCGCTCAGTACCATGAGACAGAGCGCTGCCACGAG 266
 181 ggcacagcggtgcccgcgcgcgtcagtaacatgagacagcgctgcccacgagacg 240
 267 CCAGCAATTCAGCTATGCTTGGGCTCAAGTTGCTCCCGACAGCCAGCCCGGTT 326
 241 ccagcaatctgactgtacctgtgactcaagttgtctcccaagcaccagcccggtt 300
 327 CCTGGGTAACCTTGCCCACTTATGATGGCACTGTGCGAGCCAGCGGTCCGAGCG 386
 301 cctggtaacctgtgcccaactagatgagacactgtccgacccatgcyggtccgaa 360
 387 CGGACCTGGCGGAGAGACAGCTGTGCTCCGACCGGAGTCCCTCATGATCAGG 446
 361 cggacctggcgagagagacagctgtgctccgacccgagctccctcatgatacag 420
 447 CCATACGATATAGCCCTCTACTCATGCTGTGGTGGGGCTCTCCGAATCTTC 506
 421 ccatacgatactgcccctctactccatctgctgctggtgggtctctcggaaacttc 480
 507 TGTGTCATGTATGTATGTACAGTACACCAAGATGAGAGTCCCAACATCTACATT 566
 481 tgtgtcatgtatgtatgtatgtacagatcaccaagatgaagactgcacacacatct 540
 567 TCACCTTGCTCTGGCAAGTATGCTTACCCAGTACCTGCTCCGAGTGTGAATT 626
 541 tcaaccttgctctggcagatgtcttagcaaccagtaacctgtcccttcagagtgt 600
 627 ACCTAATGGGAACATGGCCATTGGAACCATCTTTGCAAGTATGATGATCCATAG 686
 601 acctaatgggaacatggccatttggaaacatcttgcagaagatgatactcatagatt 660
 687 ACTATACATGTTCACAGCATATTCACCCCTGACACCATGATGTGATGATCATTTG 746
 661 actataacatgttccacagcatatcaccccttgcacacatggtgtgtatcatcat 720
 747 CAGTGTCCACCCCTGTCAAGGCTTATGATTCCTGACTCCCGAAATGCCAAATTA 806
 721 cagtggtccacccctgtcaaggccttagatttcgtactcccgaaatgcaaatatca 780
 807 ATGTCTGAACGTGATCTCTTTCAGCCATGTGCTTCTTATGTTTCAAGGCTACAA 866
 781 atgtctgaacgtgattcttcttcagccatgtcttctcgtlaatgttcatgctcaaa 840
 867 CAAATATACAGGCTAGGTTTCATAGATTGTACACTACATCTCTCATCCAACTGTACT 926
 841 caaatatagaggagagagagatgttgaactgaactaactctctcatcaactgttact 900
 927 GGGAAACCTGCTGAAGATCTGTGTTTCATCTTGCTTCAATTAAGCATGCTCATCA 986
 901 gggaaacctgctgaagatctgtgtttcatcttgcctctcatatgcaagtgctcatca 960
 987 TTACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1046
 961 ttaccgtgtgcatgactgactgactgactgactgactgactgactgactgactgact 1020

1047 CCAAGAAAAGACAGATCTTCGAAGATCACAGAGATGGTGTGGTGGTGGCTG 1106
 1021 ccaagaaaagacagatcttcgaagatcacagagatgggtgtgggtgggtgggt 1080
 1107 TGTTCATGCTGTGCTGAGCTCCCATTCATCAATTTACGTATCATTTAAAGCTTGTACAA 1166
 1081 tgttcattgtctgtcgtgctcccatctcatcttaacgtcatctaaagcctgtgtacaa 1140
 1167 TCCCAAGAACTACGTTCCAGACTGTTTCTTGCACTTCTGATTCCTAGTTACACAA 1226
 1141 tcccaagaaactacgttccagactgttcttctgcaacttctgacttctcctaagttacaaa 1200
 1227 ACAGCTGCTCAACCCCATCTCTTATGCAATTTCTGATGATAAACTTCAAGATGCTTCA 1286
 1201 acagctgctcaaccccatctcttattgtatcttctgagaaactcaaaagatcttca 1260
 1287 GAGAGTTGTATCCCAACCTCTTCCAACTTGAAGCAAAACTCCACTGAAATTGCTC 1346
 1261 gagagttgtatcccaacctcttccaaacttgagcaaaaactccactcgatctgc 1320
 1347 AGAAGCTAGAGACACCCCTCCACGCGCAATACAGTGATAGAACTATGATCAGCTAG 1406
 1321 agaagctagagacacccctccacgccaatacagtgatagaaactatcatcagctag 1380
 1407 AAATCTGGAAGACAAACTGCTCCGTTGCCCTAAGAGGTCTCATGCTCCGACCTT 1466
 1381 aaatctggaagacaaactgctccggttgccttaacagaggtctcatctcgaactt 1440
 1467 CACCAAGCTTGAAGCCACCATGATGTGGAAGCAGGTTGCTTCAAGATGTGAGAGG 1526
 1441 caccaagcttgaagccacccatgtatgtgaagcaggttcttcaagaatgtgtagagag 1500
 1527 CTCTAATCTCTAGGAAGTGGCTGCTTATGATCATCAACCTCTTCTCTCGGGCA 1586
 1501 ctctaattctctaggaagtggcttattgagttacccaacctcttcccttcggcca 1560
 1587 CTCTGCTCTGCACATTAAGAG 1607
 1561 ctctgctctgcacattagag 1581

RESULT 10
 ID V61989 standard; cDNA; 2162 BP.
 XX
 AC V61989;
 DT 11-JAN-1999 (first entry)
 XX
 DE Human mu-opioid receptor cDNA variant 5.
 XX
 KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
 KW predilection; addition; analgesic; anaesthetic; anti-addictive;
 KW psychopharmaceutical agent; diagnostic; site effect; drug; opiate;
 KW cocaine; inherited alcoholism; human; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 213..2040
 FT /tag- a
 FT /product- "mu-opioid receptor"
 FT 502..503
 FT /tag- b
 FT /note- "Site of Intron 1"
 FT 855..856
 FT /tag- c
 FT /note- "Site of Intron 2"
 FT 1376..1377
 FT /tag- d
 FT /note- "Site of Intron 3"
 FT mutation 229

Oy	1527	CTGTAATTCGTAGGAAGTCCGCTTTTAGGCATCCAACTCTTGCTGTCAGCA	1586
Cc			
Dd	1501	ctctaattctctgaggaagaatggccaccttttagtgcataccaactcttcctctggcca	1560
Oy	1587	CTCTGCTCTGCACATTAGAGG	1607
Cc			
Dd	1561	ctctgctctgcacattagagg	1581
RESULT	11		
ID	V61990		
XX	V61990 standard; cDNA; 2162 BP.		
AC	V61990;		
XX			
DT	11-JAN-1999 (first entry)		
XX			
DE	Human mu-opioid receptor cDNA variant 6.		
KW	Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;		
KW	predisposition; addition; analgesic; anaesthetic; anti-addictive;		
KW	psychopharmaceutical agent; diagnostic; side effect; drug; opiate;		
KM	cocaine; inherited alcoholism; human; ss.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	213..2040	
FT		/tag- a	
FT		/product- "mu-opioid receptor"	
FT		502..503	
FT		/tag- b	
FT		/note- "Site of intron 1"	
FT		855..856	
FT		/tag- c	
FT		/note- "Site of intron 2"	
FT		1376..1377	
FT		/tag- d	
FT		/note- "Site of intron 3"	
FT		330	
FT		/tag- e	
FT		/note- "Wild type A is replaced by G"	
XX			
XX	WO9833937-A2.		
XX			
PD	06-AUG-1998.		
XX			
Pf	02-FEB-1998;	98WO-DE00382.	
XX			
PR	03-FEB-1997;	97DE-1003925.	
XX			
PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.		
PI	Hoehe M, Wendel B:		
DR	WPI; 1998-437487/37.		
PT	New genomic and cDNA sequences encoding human mu-opioid receptor -		
PT	used, e.g. to predict pre-disposition to addiction and for		
XX	development of analgesics, anaesthetics and anti-addiction agents		
PS	Claim 8; Page -: 26pp; German.		
CC	This sequence encodes a novel human mu-opioid receptor in which an A		
CC	nucleotide at position 330 of the wild-type sequence represented in		
CC	V61984 is replaced by a G. The wild type receptor and its variants,		
CC	polymorphisms and mutants are used in a method for detecting		
CC	predisposition to disease, particularly additive disease, by isolating		
CC	DNA from a sample, genotyping selected positions and comparing with a		
CC	reference DNA. Such sequences are used to develop analgesic, anaesthetic,		
CC	anti-addictive and psychopharmaceutical agents, to construct genes and		

[illegible]


```

|||||
Db 841 caaatacagcgaaggtccatagatgtacacacatctctccacccaacccggaact 900
QY 927 GGGAAACCTGCTGAGATGCTGTGTTTCATCTTGGCTTCATTATGCCAGTGTCTATCA 986
Db 901 gggaaacacgtcgtgaagatctgtttcttccatcttcgccttaattatgccaagtctcatca 960
QY 987 TTACCGGTGCTATGAGTATGATGCTTGGCCCTCAAGAGTGTCCGATGCTGCTGCTGCT 1046
Db 961 ttacagtggtctatgagactgtatgtatcttcgcccacgaagatgctcgtatgctctgct 1020
QY 1047 CCAAGAAAGGAGACAGAAATCTTTCGAAGATCACACAGATGCTGCTGCTGCTGCTGCTG 1106
Db 1021 ccaagaagaagagacaggaatcttcgaagatcacagaagatgctgctgctgctgctgctg 1080
QY 1107 TGTTCATGCTGCTGCTGAGTCCCATTCATCATTTAGTTCATTTAAAGCTTGTTACAA 1166
Db 1081 tgttcacgtctgctgtgagctcccatccatccatcttaccatcaatgaagccttgcttaca 1140
QY 1167 TCCAGAAACTAGGTTCCAGACTGTTCTTGGGACTTCTGATTCGCTAGTGTACACAA 1226
Db 1141 tcccaagaacacgtctccagacgtctcttgcaccttcgactgctcctaggttacacaa 1200
QY 1227 ACAGCTGCTCAACCCAGCTCTTATGATTTCTGATGAAAACTCAAGATGCTTCA 1286
Db 1201 acagctgcctcaacccagcctcttattgcatcttcgtgatgaaactcaacagatcttca 1260
QY 1287 GAGAGTTCTTATCCCACTCTTCCAACTGAGCAAAACTCCACTCGAATGTGCTC 1346
Db 1261 gaggtctgtatcccaactcttccaacattgagcaaaaactccactcgaattcgtc 1320
QY 1347 AGAAGACTAGAGCCACCCCTCCACGGCCAAATAGAGTAGAATCATCATAGCTAG 1406
Db 1321 agaacactaagagaccacctccacgccaatagacgtggaagaactcaatcaatcagctag 1380
QY 1407 AAAATCTGGAAGCAGAAACTGCTCCGCTTAACAGGGTCTCATGCCATTCGGACCTT 1466
Db 1381 aaatctcggaagcagaacacgtctcgttcgtccctaaagaggtctcattcgacactc 1440
QY 1467 CACCAAGCTTAGAAGCCACCATGATGATGAGAGCAGGTTGCTTACGAATGTGAGAGG 1526
Db 1441 caccaaagcttagaagcaccacatgatatggaagcaggtctgcttaagaatgtgtagag 1500
QY 1527 CTCTAATCTCTAGGAAGTGCCTTTTAGTGCATCCAACTTCCCTGCTGGCCA 1586
Db 1501 ctctaaatctctaggaagatgaccttaagcttaagctcaacacctcttcctctgcca 1560
QY 1587 CTCTGCTCTGCACATTAGAGG 1607
Db 1561 ctctgctctgcaacttagag 1581

RESULT 12
V61991
ID V61991 standard; cDNA; 2162 BP.
XX
AC V61991;
DT 11-JAN-1999 (first entry)
XX
DE Human mu-opioid receptor cDNA variant 7.
XX
KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW prediagnosis; addition; analgesic; anaesthetic; anti-addictive;
KW psychopharmacological agent; diagnostic; side effect; drug; opiate;
KW cocaine; inherited alcoholism; human; ss.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 213..2040
FT /tag= a

```

```

FT misc_feature /product= "mu-opioid receptor"
FT 502..503
FT /tag= b
FT /note= "Site of intron 1"
FT misc_feature /tag= c
FT 855..856
FT /note= "Site of intron 2"
FT misc_feature /tag= d
FT 1376..1377
FT /note= "Site of intron 3"
FT mutation
FT 666
FT /tag= e
FT /note= "Wild type A is replaced by G"
W09833937-A2.
PD 06-AUG-1998.
PF 02-FEB-1998; 98MO-DE00382.
PR 03-FEB-1997; 97DE-1003925.
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX Hoehe M, Wendel B;
XX WPI; 1998-437487/37.
XX
XX New genomic and cDNA sequences encoding human mu-opioid receptor -
XX PT used, e.g. to predict pre-disposition to addiction and for
XX development of analgesics, anaesthetics and anti-addiction agents
XX
XX Claim 8; Page -: 26pp; German.
XX
XX This sequence encodes a novel human mu-opioid receptor in which an A
XX nucleotide at position 666 of the wild-type sequence represented in
XX V61984 is replaced by a G. The wild type receptor and its variants,
XX polymorphisms and mutants are used in a method for detecting
XX prediagnosis to disease, particularly addictive disease, by isolating
XX DNA from a sample, genotyping selected positions and comparing with a
XX reference DNA. Such sequences are used to develop analgesic, anaesthetic,
XX anti-addictive and psychopharmacological agents, to construct genes and
XX vectors, particularly for pharmaceutical development, to develop
XX diagnostic kits for predicting risk of addiction, response to analgesics
XX or anaesthetics, or development of side effects from a drug. Particula-
XX applications are to determine risk of addiction to opiates or cocaine, or
XX of developing inherited alcoholism.
XX CC Note: This sequence is not represented in the specification and has
XX been constructed from the wild-type sequence represented in V61984 in
XX accordance with the specification.
XX
XX Sequence 2162 BP; 561 A; 565 C; 459 G; 575 T; 2 other;
SQ

Query Match 74.8%; Score 1205; DB 19; Length 2162;
Best Local Similarity 99.6%; Pred. 0;
Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

```


XX Claim 8: Page 7: 26bp; German.
 PS
 XX

CC This sequence encodes a novel human mu-opioid receptor in which a G
 CC nucleotide at position 1006 of the wild-type sequence represented in
 CC V61984 is replaced by an A. The wild type receptor and its variants,
 CC polymorphisms and mutants are used in a method for detecting
 CC predisposition to disease, particularly addictive disease, by isolating
 CC DNA from a sample, genotyping selected positions and comparing with a
 CC reference DNA. Such sequences are used to develop analgesic, anesthetic,
 CC anti-addictive and psychopharmaceutical agents, to construct genes and
 CC vectors, particularly for pharmaceutical development, to develop
 CC diagnostic kits for predicting risk of addiction, response to analgesics
 CC or anaesthetics, or development of side effects from a drug. Particular
 CC applications are to determine risk of addiction to opiates or cocaine, or
 CC of developing inherited alcoholism.
 CC Note: This sequence is not represented in the specification and has
 CC been constructed from the wild-type sequence represented in V61984 in
 CC accordance with the specification.
 XX

SO Sequence 2162 BP; 563 A; 565 C; 457 G; 575 T; 2 other:

Query Match 74.8%; Score 1205; DB 19; Length 2162;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 28 TGGGAGGGGCTATACGACAGAGAGATGTCATGCTCAGCTGCTCCCTCCGCTGA 87
 DB 1 TGGGAGGGGCTATACGACAGAGAGATGTCATGCTCAGCTGCTCCCTCCGCTGA 60
 QY 88 CGCTCCTCTGCTCAAGCCGAGCTGCTTCTGTAAGAAACAGAGAGCTGGGAGC 147
 DB 61 CGCTCCTCTGCTCAAGCCGAGCTGCTTCTGTAAGAAACAGAGAGCTGGGAGC 120
 QY 148 GGCAGAAAGAGAGCGCTGAGCGCTTGAGAACCGAAAGTCTGGTGTCTTGGTACT 207
 DB 121 GGCAGAAAGAGAGCGCTGAGCGCTTGAGAACCGAAAGTCTGGTGTCTTGGTACT 180
 QY 208 CGCAGACG-GTGGCCGCGCGCGCTGAGTACATGAGACAGAGCGCTGCGGAGAGC 266
 DB 181 CGCAGACG-GTGGCCGCGCGCGCTGAGTACATGAGACAGAGCGCTGCGGAGAGC 240
 QY 267 CCACGATTTGATGATGATGCTTGGCTGATGATGCTTGGCTGATGATGATGATGAT 326
 DB 241 CCACGATTTGATGATGATGCTTGGCTGATGATGCTTGGCTGATGATGATGATGAT 300
 QY 327 CTTGGTCAACTTGTCCACTTGAATGAGCAACTGTCCGACCATGCGGTCCGAGC 386
 DB 301 CTTGGTCAACTTGTCCACTTGAATGAGCAACTGTCCGACCATGCGGTCCGAGC 360
 QY 387 CGGACCTGGGCGGAGAGACAGCTGTGCTCCGACCGGAGTCCCTCATGATCAGG 446
 DB 361 CGGACCTGGGCGGAGAGACAGCTGTGCTCCGACCGGAGTCCCTCATGATCAGG 420
 QY 447 CCATCAGCATGATGATGCTTACTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 506
 DB 421 CCATCAGCATGATGATGCTTACTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 507 TGGTCACTGATGATGATGCTGATACACAGATGAGACTGCGCAACATCTCATATT 566
 DB 481 TGGTCACTGATGATGATGCTGATACACAGATGAGACTGCGCAACATCTCATATT 540
 QY 567 TCAACCTTGTCTGGAGATGCTTACGACACAGTACCTGCTTCCAGAGTGAATT 626
 DB 541 TCAACCTTGTCTGGAGATGCTTACGACACAGTACCTGCTTCCAGAGTGAATT 600
 QY 627 ACCTAATGGAGACATGAGCATTTGAAACCATCTTTGCAATATGATGATCCATAGAT 686
 DB 601 ACCTAATGGAGACATGAGCATTTGAAACCATCTTTGCAATATGATGATCCATAGAT 660
 QY 687 ACTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 746
 DB 661 ACTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT

DB 661 actataacatgttcaccagcatattcacccctcgcacattgagtggtgatcatatg 720
 QY 747 CAGTCTGCCACCCCTGTAAGGCTTATGATTTCCGTACTCCCGCAAAATGATATCA 806
 DB 721 cagtcctcccccgttaagagccttagattccgtactcccgaaatgcaaaattatca 780
 QY 807 ATGCTCAACTGATGATGCTTCTTCCAGCAATGCTTCCGTAATGTCATGCTCAAA 866
 DB 781 atgctcaactgatactctctctccagcattgtctctctgtatgtatgtatcaaa 840
 QY 867 CAATATCAGGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 926
 DB 841 caaatatcaggaagatgattgattgattgattgattgattgattgattgattgattgatt 900
 QY 927 GGGAAACCTGCTCAATATGCTTTCATCTTCCCTTATATGCAAGTGTCTATCA 986
 DB 901 gggaaacctgtgaagatcgtgtttcattcttcgcttcatattgacagtgctatca 960
 QY 987 TTACGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1046
 DB 961 ttaccgtgtctatgagctatgattctcgtcccaagagtgccacatgctctcgtgct 1020
 QY 1047 CCAAGAAAGAGACAGATTTTGAAGATCACAGAGATGCTGCTGCTGCTGCTGCTG 1106
 DB 1021 ccaagaaagagacaggaatcttcgaagatccacagagatggtgtgtgtgtgtgtgtgt 1080
 QY 1107 TGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1166
 DB 1081 tgttcacgt 1140
 QY 1167 TCCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1226
 DB 1141 tccagaaatgagcttccagagatcttcgaagatccacagagatggtgtgtgtgtgtgt 1200
 QY 1227 ACAGCTGCTCAACCCAGTCTTATGATGATGATGATGATGATGATGATGATGAT 1286
 DB 1201 acagctgctcaacccagcttcttatgattctgtgtgtgtgtgtgtgtgtgtgtgtgt 1260
 QY 1287 GAGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1346
 DB 1261 gagagctgtgattccaaacctctccaaacttgagcaaaactccactcgaattcgtc 1320
 QY 1347 AGAAGCTAGAGACACACCCCTCCAGGCAATACAGTGTAGATGATGATGATGAT 1406
 DB 1321 agaagctagagaccacctcccaagccatacagatgagatgagatgagatgagatgag 1380
 QY 1407 AAATCTGGAAGCAAACTGCTCCGTTGCCCTTAACAGGGTCTCATGCCATTCG 1466
 DB 1381 aaatctggaagcagaactgctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440
 QY 1467 CACCAAGCTTAGAAGCCATGATGATGATGATGATGATGATGATGATGATGATGAT 1526
 DB 1441 caccaagcttagaagccacatgattgtgaaagagtgcttcaagaatgattgagag 1500
 QY 1527 CTTAATTTCTTAGAAGTGGCTGCTTTAGGTCATGCAACCTTCCCTGCTGGCA 1586
 DB 1501 cttaattcttagaagtgccactttagtgcatacccaacctctctctctctgtgcca 1560
 QY 1587 CTCTGCTCTGCTACATTTAGAGG 1607
 DB 1561 ctctgctctgacattagagg 1581

RESULT 14
 V61993
 ID V61993 standard; cDNA: 2162 BP.
 XX
 AC V61993;
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Human mu-opioid receptor cDNA variant 9.
 XX

XX		Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KW		predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KM		psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KX		cocaine; inherited alcoholism; human; ss.
OS	Homo sapiens.	
OS	Synthetic.	
XX		
XX	Key	Location/Qualifiers
FT	CDS	213..2040
FT		/tag- a
FT		/product- "mu-opioid receptor"
FT	misc_feature	502..503
FT		/tag- b
FT	misc_feature	855..856
FT		/tag- c
FT		/note- "Site of intron 2"
FT	misc_feature	1376..1377
FT		/tag- d
FT		/note- "Site of intron 3"
FT	mutation	1014
FT		/tag- e
FT		/note- "Wild type T is replaced by C"
XX		
PN	MO9833937-AZ.	
XX		
XD	06-AUG-1998.	
XX		
XX	02-FEB-1998;	98WO-DE00382.
PF	03-FEB-1997;	97DE-1003925.
PR		
XX	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
PA		
P1	Hoehne M, Wendel B;	
XX		
DR	WPI: 1998-437487/37.	
XX		
PT	New genomic and cDNA sequences encoding human mu-opioid receptor -	
PT	used, e.g. to predict pre-disposition to addiction and for	
PT	development of analgesics, anaesthetics and anti-addiction agents	
XX		
PS	Claim 8; Page -: 26pp; German.	
XX		
CC	This sequence encodes a novel human mu-opioid receptor in which a T	
CC	nucleotide at position 1014 of the wild-type sequence represented in	
CC	V61984 is replaced by a C. The wild type receptor and its variants,	
CC	polymorphisms and mutants are used in a method for detecting	
CC	predisposition to disease, particularly addictive disease, by isolating	
CC	DNA from a sample, genotyping selected positions and comparing with a	
CC	reference DNA. Such sequences are used to develop analgesic, anaesthetic,	
CC	anti-addictive and psychopharmaceutical agents, to construct genes and	
CC	vectors, particularly for pharmaceutical development, to develop	
CC	diagnostic kits for predicting risk of addiction, response to analgesics	
CC	or anesthetics, or development of side effects from a drug. Particular	
CC	applications are to determine risk of addiction to opiates or cocaine, or	
CC	of developing inherited alcoholism.	
CC	Note: This sequence is not represented in the specification and has	
CC	been constructed from the wild-type sequence represented in V61984 in	
CC	accordance with the specification.	
XX		
XQ	Sequence 2162 BP; 562 A; 566 C; 458 G; 574 T; 2 other;	

```

Query Match 74.8%; Score 1205; DB 19; length 2163;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1.

QY 28 TGGAGGGGGGCTATACGCAGAGAGAGATTCAGATGCTCGGTCCCTCCGCGCTGA 87
|||||
Db 1 tggaggggggctatcgcagagagaaatgtctcagatgctcgtccctcccgccctga 60

```

OY	88	CGCTCTCTCTGCTCTCAGCCAGCAGACTGGTTTCTGTAAGAAACAGCAGAGGCTGTGGCAGC	147
Db	61	cgctctctctcgtctcaagccagacccggtttctctgtaaagaacaagaagcgctgtgagcgc	120
OY	148	GGCGAAAGAGAGCGGCGTGAAGCGCCTTGGAAACCGAAACTCTCGTGCTCTGCTACT	207
Db	121	ggcgaaagaagcgcgctgtgaagcgctcttggaaccggaaaatctctggtctcctgtgtaact	180
OY	208	CGCACAGC- g ggcccccggccggcggtcagTAACATACATAGACACGAGCGCTGGCCCCACGAGC	266
Db	181	cgcacaagcggtgtgcccgcgcggtccggtcaagtaaccatgtgacacgacgctgcccccaagaa	240
OY	267	CCAGCAATTGCATCGATGCTTGGCGCTACTCAAATTGCTCCCAACACCCACGCCGGTT	326
Db	241	ccaagaattgactgactgtccttggtcgtaactcaagttgtctcccaagaaccagccccggtt	300
OY	327	CGTGGGTCACATTGTCCCACTTGTAGTAGGAACCTGTGCGACCCATGCGGTCCGAAACGCA	385
Db	301	ccctgggtcaactgtgccacttagaagcaaccgtgtccgaaccgaagcggtgtccgaacgcga	360
OY	387	CCGACCTGGGGGGAGAGACAGCCTGTGCCTTCCAGCCGGCAGTCCCTCATGATACAGG	446
Db	361	ccaacctggggggagagagacagcgtgtgccctccgacgcgcaagtccctcatgtacaggt	420
OY	447	CCATTCAGATCATGCGCCTTACTCATGTGTGTGCGTGTGGGCTCTTGGAAACTTCC	506
Db	421	ccatcagatcatatgtccccttactcatcagtgtgcgtgtgggtgtccttcggaaaattcc	480
OY	507	TGGTCATGTAATGATTTGTGAGATATACACCAAGATGAAGACTCCACCAACATCTCATTT	566
Db	481	tgtgtcatgtatgtatgtgtcagaataacccaagaatgaagacgtgcacacaacatctcaatt	540
OY	567	TCAACTTGTGCTGTGGCAGATGCTTAGCCACACAGTACCCCTGCTCCAGAGTGAATT	626
Db	541	tcaacctgtgcctctgcagatgaccttagccaaccagtccccctgcccaagtgtaatt	600
OY	627	ACGTAATGGGAAACATGGCCATTGGAAACCATCCTTGGCAAGTAGAGATCCATAGATT	686
Db	601	acctaaatgggaacatgtgccttgggaacatccttggcaagtagtgatctccataagttc	660
OY	687	ACTATACATGTTTACACAGCATATTTACCCCTGACCAATGATGTTGATGATCATTTG	746
Db	661	actatacatgttcaaccagataataccacctgtgcacaaatgagtgtgatcgatacatgt	720
OY	747	CAGTCTCCACCCCTGTCAAGCCTTAGATTTCGTACTCCCCGAAGTCCAAAAATTATCA	806
Db	721	cagttctccaccctcgctaaagcccttagattccgtatctccgaatgtccaaaattatca	780
OY	807	ATGCTCTCACTGGATCCTCTCTTACAGCATTGCTTCTCTTAATGTTCAATGAGCTTACA	866
Db	781	atgtctgcaactgtatctctctctctcaagcatgtgtcttcctgttaatgttcaatgtctaa	840
OY	867	CAAAATACAGGCAAGGTTCCATAGATTGTACACTTAACATTTCTCTATCCAACTGTACT	926
Db	841	caaaatcacaggcaaggttccatagattgtacatacaatctctcatccaacctgtact	900
OY	927	GGGAAACCTCGTAGAGATGTGTTTATCTGTCCCTCAATTATGACAGAGTCAATCA	986
Db	901	gggaaaacctcgtggaagatctgtttcatcaatcttgccttcaatgtccgaatgtcatca	960
OY	987	TTACCGTGTCTATGACATGATGATCTTGCGCTCAAGAGTCCGCAATGCTCTTGACT	1046
Db	961	ttaccgtgtctatgtagactgtatctcttggtccctcaaggtgtccgaatgtctccctggt	1020
OY	1047	CCAAAGAAAAGGACGGAATCTTCGAAGATATACCAAGATGCTGTGTGTGTGGCTG	1106
Db	1021	ccaaagaaaaggacggaactcttcgaagatcatcaacgaatgtgtgtgtgtgtgtgtgtgt	1080
OY	1107	TGTTATCTGCTCTGTGAGACTCCCATTCACATTTAGTCACTATTAAACCTTGGTTAAAC	1166
Db	1081	tgttcatctgtctgtgactcccatctcaatctaagtgatcatctaagaaccttgtgtataaa	1140
OY	1167	TCCCAAGAACTACGTTCCAGACTGTTTCTTGGCACTTTCGATTCGCTCTAGGTTACACAA	1226

[illegible]

RESULT	15
V61994	
ID	V61994 standard; cDNA: 2162 BP.
XX	
XX	V61994;
AC	
DT	11-JAN-1999 (first entry)
DE	Human mu-opioid receptor cDNA variant 10.
XX	
KM	Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;
KM	predisposition; addiction; analgesic; anaesthetic; anti-addictive;
KM	psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KM	cocaine; inherited alcoholism; human; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	213..2040
FT	/tag= a
FT	/product= "mu-opioid receptor"
FT	502..503
FT	/tag= b
FT	/note= "Site of intron 1"
FT	855..856
FT	/tag= c
FT	/note= "Site of intron 2"
FT	1376..1377
FT	/tag= d
FT	/note= "Site of intron 3"
FT	1154
FT	/tag= e
FT	/note= "Wild type G is replaced by A"
PN	WO9833937-AZ.
XX	
XX	06-AUG-1998.
PD	
XX	
XX	02-FEB-1998; 98WO-DE00382.

PR 03-FEB-1997; 97DE-1003925.
XX
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Hoehe M, Wendel B;
XX
XX WPI; 1998-437487/37.
DR

PT New genomic and cDNA sequences encoding human mu-opioid receptor
PT used, e.g. to predict pre-disposition to addiction and for
PT development of analgesics, anaesthetics and anti-addiction agents
XX
PS
PS Claim 8; Page -; 26pp; German.

Claim 8; Page -; 26pp; German.

CC This sequence encodes a novel human mu-opioid receptor in which a G
CC nucleotide at position 1154 of the wild-type sequence represented in
CC V61984 is replaced by an A. The wild type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic, anaesthetic,
CC anti-addictive and psychopharmaceutical agents, to construct genes and
CC vectors, particularly for pharmaceutical development, to develop
CC diagnostic kits for predicting risk of addiction, response to analgesics
CC or anaesthetics, or development of side effects from a drug. Particular
CC applications are to determine risk of addiction to opiates or cocaine, or
CC of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in V61984 in
CC accordance with the specification

Sequence 2162 BP; 563 A; 565 C; 457 G; 575 T; 2 other;

Query Match	74.8%;	Score 1205;	DB 19;	Length 2162;
Best Local Similarity	99.68;	Pred. No. 0;		
Matches 1575;	Conservative	0;	Mismatches 5;	Indels 1;
			Gaps	1;

QY	28	TGGGAGGGGG- <u>TTATACCAGAGAGAGATGTCATGCTCAGCTCGATCGCTCCGACCTGA</u>	87
Db	1	ttggaaagggggtctaaagcagagaggaatgtctcagatgtctcagctctcggtccctccgcttga	60
QY	88	CGCTCTCTCTGTCTCAGCCAGAGACTGTTCTGTAAAGAAACAGACAGAGCTGTGGAGC	147
Db	61	cgcctccctctcgtctccagccagagactggtttctgttaagaaacagcagagactgtgycagc	120
QY	148	GGCGAAAGGAAGCGCGGTGAGGGCGTTTGGAACCCGAAAAGTCTGGTGTCTCTGGCTACCT	207
Db	121	ggcgaaaggaagcgcgtctgaagtcgctctggaaccgaaatctcgtgtctcctgtctactc	180
QY	208	CGCACAGC -GTGCCCGCCCGGCCCTCAGTACCATGAGACAGAGCGCTGCCCCACGAAAGC	266
Db	181	cgacacagcgtgtgccgcgcgcgcgtctcagtaaccatgtgacagcagcgtctgccccacgaagc	240
QY	267	CCACAGCATTTGACAGATGATCTGGCGGTACTCAATTTCTCTCCAGACACCAGCCCGGTT	328
Db	241	ccagcaatctgacactgactgtcccttggcgtactcaagtgtctcccaagcaccagccccggtt	300
QY	327	CGTGGGTCAACTTGTCCCACTTAATGGAACCGTTCGACCCCATGGCGGTCCGAACCGCA	388
Db	301	cttgggtccaacttgtctccacttagatgtgcaaccctgtccgaaccatgtggtctcgaaaccga	360
QY	387	CCGACCTGGGCGGGAGAGACAGCCTGTGCCCTCCGACCGGCAGTCTCCTCATGATCAGG	448
Db	361	ccaacacttgggctgggagagaaacagctgtgcccctccgacacggcagctccctccatgatacag	420
QY	447	CCATCAGAGATATGAGCCCTTACTCCATCGTGTGCCGTGGTGGGGCTTTGGGAAACTTCC	505
Db	421	ccatcaacgatactgagccctctactccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	480
QY	507	TGGTCATGTATGTATGTGTGATGATACCAAGATGAAGACTGCCACCAACATCTACTATT	566
Db	481	tgtgcatgtatgtatgtatgtcatgaatacccaagatgaagactgtccacaaatctaacattt	540

```

QY 567 TCAACCTTGCTGAGATGCTTAGCCACAGTACCGCTTCCAGAGTGTAAAT 626
Db 541 tcaaccttgctcgagatgcttagccacagtagaccttccagagtggaatt 600
QY 627 ACCTAATGGGAACATGGCCATTGGAGCAATCCTTTGCAAGATAGTATCTTCATGAT 686
Db 601 acctaatgggaacatggccattggagcaatcctttgcaagatagtagtctccatagatt 660
QY 687 ACTATACATGTTCCACGACATATTCACCCCTGACCATGATGATGATGATGATGATG 746
Db 661 actataacatgttccacgacatattcacccctcgaccatgagtgtgtatcgatcatgt 720
QY 747 CAGTGTGCACCCCTGCAAGGCTTGAATTCAGTACTCCCGAATGCAAAATATATCA 806
Db 721 cagtgctcacccctgcaaggcttgaattcagttaccccgaaatgcaaaatlatca 780
QY 807 ATGCTGCAACTGATGATCTCTCTTACGCCATTGCTCTCTGTAATGTTCAATGCTTACA 866
Db 781 atgctgcaactgatgattctcttaccatgtgtcttccctgtaattgttcatggttaca 840
QY 867 CAAATACAGCAAGGCTTCATAGATTTGACACTAACATTTCTCTATCCAACTGCTACT 926
Db 841 caaatacagcaaggcttcattagatttgacactaacatttctctatccaaactgttact 900
QY 927 GGGAAACCTGCTGAGATCTGTTTTCATCTTCCCTCATATATGCGAGTGCATCA 986
Db 901 gggaaacctgctgagatctgttttcattcttccctcatatttgcagtgctcatca 960
QY 967 TTACCGTGTCTANGAGTATGATCTTGCGCTCAAGAGTGCAGATGCTCTGTGCT 1046
Db 941 ttaccgtgtctangagtattgattcttgccgctcaagagtgcagatgctctgtgct 1020
QY 1047 CCAAGAAAGAGGAGCATCTTGAAGATCAGAGATGCTGAGTGGTGGTGGTGGTGG 1106
Db 1021 ccaagaaagagagcatcttgaagatcagagatgagtgatggtgggtgggtgg 1080
QY 1107 TGTTCATGCTGCTGAGTCTCCATTCATTTACATTTAAAGCTTGTGTTACAA 1166
Db 1081 tgttcattgctgctgagctcccatcattcaatttaagcttcaatcaagcttgttaca 1140
QY 1167 TCCCAAGAACTAGCTTCAGACTGTTTCTTGGCACTTGTGCTGCTGCTGCTGCTGCT 1226
Db 1141 tcccaagaaactagcttccagactgtttcttggcaacttgccttgcctcaggttaca 1200
QY 1227 ACAGTGTCTGCTAAGCCATCTTATGATTCGATGGAATCAAACTCAAGATGCTTCA 1286
Db 1201 acagtgtctcaagccatcttattgattcttggatgaaactcaagatgcttca 1260
QY 1287 GAGAGTCTGTATCCCACTCTTCCCAATTTGACCAACAAACTCACTGATTTGCTC 1346
Db 1261 gagagtctgtatcccaactcttcccaatgttgcacaaactccactgtaattctgc 1320
QY 1347 AGAACACTAGAGACACCCCTCCACGCGCATACAGTGAATGAATATCATCGCTAG 1406
Db 1321 agaacactagagacacccctccacgcgcaatacagtgatagaactaatactcagctag 1380
QY 1407 AAAATCTGAGAGCAGAACTGCTCGTTCGCTTACAGAGGTGCTCATGCTATTCGACCTT 1466
Db 1381 aaaatctgagagcagaaactgctcgcttgcctcaagaggtctcatgcatccgaacct 1440
QY 1467 CACCAAGCTTGAAGCCACCATGTATGTGAAGCAGGTTGCTTCAAGATGTGTGAGAG 1526
Db 1441 caccaagcttgaagccaccatgtatgtggaagcaggttgcctcaagatgtgtgagag 1500
QY 1527 CTCTAATTTCTTAGAAGTGCCTGCTTTAGGTCATCCAACTCTTCTCTGCGCA 1586
Db 1501 ctctaatttcttagaagtgcctgcttttaggtcatccaactcttctctctcgtgca 1560
QY 1587 CTCTGCTCTGCACATTAAGG 1607
Db 1561 ctctgctctgcacattagagg 1581

```

```

RESULT 16
X59781
ID X59781 standard; DNA; 441 BP.
XX
AC X59781;
XX
DT 26-JUL-1999 (first entry)
XX
DE DNA encoding a mu3 opiate receptor protein.
XX
KW Mu1 receptor; agonist; antagonist; mu3 opiate receptor; vasculitis;
KW cannabinoid receptor; estrogen surface receptor; arthritis; pericarditis;
KW intracellular calcium level; nitric oxide release; cancer; inflammation;
KW lupus; bronchitis; phrenitis; sepsis; septic shock; viral infection;
KW cardiovascular disease; atherosclerosis; ss.
XX
OS Homo sapiens.
XX
PN M09924471-A1.
XX
PD 20-MAY-1999.
XX
PE 10-NOV-1998; 98MO-US23944.
XX
PR 10-NOV-1997; 97US-0065043.
XX
PA (UYNV ) UNIV NEW YORK STATE RES FOUND.
XX
PI Fulmini C, Stefano GB;
XX
WP1: 1999-337698/28.
XX
DR P-PSDB; Y15470.
XX
PT Identifying modulators of opiate, cannabinoid and estrogen receptors
XX
PS Claim 49; Page 22; 79pp; English.
XX
CC The present sequence encodes a mu3 opiate receptor protein. The
CC specification describes methods for identifying agonists
CC and antagonists of mu3 opiate, cannabinoid (CAN) and estrogen surface
CC (ES) receptors. The agonists and antagonists modulate intracellular
CC calcium levels and/or release of nitric oxide from cells. The
CC antagonists are used to treat cancer (carcinoma, leukemia, melanoma,
CC cancer of the breast, lung, prostate, colon). Agonists are used to treat
CC inflammation including arthritis, pericarditis, vasculitis, lupus,
CC bronchitis and phrenitis; sepsis/septic shock; viral, including human
CC immune deficiency, infections; and for agonists of ES only,
CC cardiovascular disease, particularly atherosclerosis.
XX
SO Sequence 441 BP; 110 A; 115 C; 91 G; 125 T; 0 other;

Query Match 27.4%; Score 441; DB 20; Length 441;
Best Local Similarity 100.0%; Pred. No. 5,6e-210;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 921 GGTCTGGGAAGCACTGCTGAAGATCTGTGTTTCATCTTCCCTTATTTGCGACGTGC 980
Db 1 ggtctgggaagcaactgctgaagatctgtgtttcatcttgccttcaattatgccaagtc 60
QY 981 TCATCATACCGTGTGCTATGAGATGATCTTGCAGCTTCAAGAGTGTCCGATGCTCT 1040
Db 61 tcatcataccgtgtgtctatgagatgattcttgcagcttcaagagtgtccgactgctct 120
QY 1041 CTGCTCCAAAGAAAGACAGAACTCTTGAAGATCACAGAGATGCTGCTGTGCTG 1106
Db 121 ctgctccaaagaaagacagaaactcttgaagatcacaccagatggtgtgtgtgtg 180
QY 1101 TGGCTGTGTTATGCTGTGCGACTCCCATTCACATTATAGTATATTAACCTTGG 1160
Db 181 tggctgtgttatgctgtgcgactcccatcttcaattatagtatatttaaccttgg 240

```

```

QY 1161 TTACATCCGAGAACTACGTTCCAGACTGTTCTTGCGACTTCTGCATTCGCTAGTT 1220
DB 241 ttaaaacccagaaacacagctcccaagctgtctcttgccactctgcattgctcaggtc 300
QY 1221 ACACAAACAGCTGCGCTCACCACCACTCTTATGCAATTCGATGATAAACTTCAAGAT 1280
DB 301 acaacaacagctgcctcaaccagctccttatgattccttgatgataaactcaaacgat 360
QY 1281 GCTTCAGAGAGTTGTGATCCCAACCTCTTCCAACTGAGCAACAACTCCTCGAA 1340
DB 361 gcttcagagagttctgtatcccaacctcttcacacattgagcaacaacatccactcgaa 420
QY 1341 TTGCTCAGAACACTAGAGACC 1361
DB 421 ttcgtcagaaacactagagacc 441

RESULT 17
ID Q56703 standard: DNA; 829 BP.
XX
AC Q56703:
XX
DT 15-SEP-1994 (first entry)
XX
DE Partial sequence of the human mu opiod receptor
DE genomic clone H20 (MORA).
XX
KM Opioid receptor: morphine; opiate; ss.
XX
OS Homo sapiens.
XX
PN M09404552-A.
XX
PD 03-MAR-1994.
XX
PF 13-AUG-1993: 93MO-US07665.
XX
PR 13-AUG-1992: 92US-0929200.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
XX
DR WPI: 1994-083099/10.
XX
PT DNA encoding opiod receptors and antibodies against this
PT receptor - used to express and locate these receptors, and screen
PT cpds. for opiod (ant)agonist activity
XX
PS Example: Fig 8c: 74pp: English.
XX
CC To isolate opiate receptor genomic clones, 300,000 human genomic
CC clones and a similar number of mouse genomic clones were probed
CC with the 1.1 kb mouse delta opiod receptor clone DOR-1 Pst/XbaI
CC fragment. One mouse clone and three human genomic clones were
CC isolated. The 3 human clones had very different EcoRI patterns
CC which indicated that three different genes were represented by the
CC human genomic clones which were designated H3, H14 and H20. H20 maps
CC to chromosome 6. It encodes the human mu receptor. In addition, H20
CC appears to contain a CACACA marker (Q56704) which provides a means
CC to track the inheritance of this gene.
XX
SQ Sequence 829 BP; 182 A; 205 C; 134 G; 214 T; 94 other;

Query Match 24.3%: Score 392; DB 15; Length 829;
Best Local Similarity 100.0%: Pred. No. 1.5e-185;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 882 GTTCATAGATTGACTAATCAATCTCTCATCCAACTGCTACTGGGAAAACCTGCTGA 941
DB 369 gtccatagattgactaatactctctcatccaacctgtactgggaaaacctgctga 428

```

```

QY 942 AGATCTGTGTTTCATCTTGCGCTTCATATGCGACGCTCATCATTTACCGTGTGCTATG 1001
DB 429 agactgtgtttcatcttgcccttcattatgccagtgctcattaccggtgtcattg 488
QY 1002 GACTGATGATCTTGCGGCTCAAGAGTGTCCGATGCTGTGCTCCCAAGAAAGAGCA 1061
DB 489 gactgatgatcttgccgctcaagagtgctccgatgctcttgctccaaagaagagaca 548
QY 1062 GGAATCTTGCAAGAGTACACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1121
DB 549 ggaatcttgcaagagtaccagagatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 608
QY 1122 GGACTCCATTACATTTAGCTCATCTTAAAGCTTGTTTAAATCCCGAAACTACGT 1181
DB 609 ggactccattacatttaagctcattaaagcttggttaacaaatccagaactcagt 668
QY 1182 TCCAGACTGTTTCTTGCGACTTGTGCTGCTAGGTACACAAACAGCTGCTCAAC 1241
DB 669 tccagactgtttcttgccacttctgcattctgctaggttacacaacagctgctcaac 728
QY 1242 CAGTCTTTATGCAATTCGATGAGAAACTTC 1273
DB 729 cagtccttatgacttctgtagtaaaccttc 760

RESULT 18
ID 260733 standard: cDNA; 268 BP.
XX
AC 260733:
XX
DT 16-MAY-2000 (first entry)
XX
DE Murine mu-opioid receptor splice variant MOR-1 cDNA fragment 273051C.
XX
KM Mu-opioid receptor: MOR-1; splice variant; morphine analgesia;
KM opiod-mediated ingestive response; opiod activity; analgesic;
KM gastrointestinal motility; respiration; immune system;
KM endocrine system; autonomous nervous system; peristalsis regulator;
KM body weight; neuroendocrine disorder; ds.
XX
OS Mus sp.
XX
PN M0200004046-A2.
XX
PD 27-JAN-2000.
XX
PF 15-JUL-1999: 99MO-US15974.
XX
PR 16-JUL-1998: 98US-0092980.
XX
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
PI Pasternak G, Pan Y;
XX
DR WPI: 2000-182402/16.
XX
PT New splice variants of the mu-opioid receptor, useful in screening for
PT selective analgesics and for regulating morphine analgesia or body
PT weight -
XX
PS Claim 86; Fig 23; 83pp: English.
XX
CC The present sequence represents a fragment of a murine mu-opioid receptor
CC (MOR-1) splice variant. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opiod-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opiod activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomous nervous systems, e.g. regulators of peristalsis.

```

CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
SQ Sequence 268 BP; 73 A; 77 C; 55 G; 63 T; 0 other;

Query Match 3.7%; Score 59; DB 21; Length 268;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCGACCAACATCTACATTTTCACCTTGCTGCGAGATGCTTAGCCAC 597
|||||
DB 194 atgaagactgcccacacatctacatttcaacctgtctgcagatgcttagccac 252

RESULT 19
Z60727
ID Z60727 standard; cDNA; 1238 BP.
XX
AC Z60727;
XX
DT 16-MAY-2000 (first entry)
XX
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1G.
XX
KM Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
KM opiate-mediated ingestive response; opioid activity; analgesic;
KM gastrointestinal motility; respiration; immune system;
KM endocrine system; autonomous nervous system; peristalsis regulator;
KM body weight; neuroendocrine disorder; MOR-1G; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 18..1097
FT /*tag= a
FT /product= "MOR-1G"
XX
PN WO200004046-A2.
XX
PD 27-JAN-2000.
XX
PE 15-JUL-1999; 99MO-US15974.
XX
PR 16-JUL-1998; 98US-0092980.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Pasternak G, Pan Y;
XX
DR WPI; 2000-182402/16.
DR P-PSDB; Y68878.
XX
PT New splice variants of the mu-opioid receptor, useful in screening for
PT selective analgesics and for regulating morphine analgesia or body
PT weight -
XX
PS Claim 38; Fig 2b; 83pp; English.

CC The present sequence encodes a murine mu-opioid receptor (MOR-1)
CC splice variant MOR-1G. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine

CC or autonomous nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
SQ Sequence 1238 BP; 319 A; 343 C; 266 G; 310 T; 0 other;

Query Match 3.7%; Score 59; DB 21; Length 1238;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCGACCAACATCTACATTTTCACCTTGCTGCGAGATGCTTAGCCAC 597
|||||
DB 195 atgaagactgcccacacatctacatttcaacctgtctgcagatgcttagccac 253

RESULT 20
Z60730
ID Z60730 standard; cDNA; 1257 BP.
XX
AC Z60730;
XX
DT 16-MAY-2000 (first entry)
XX
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1H.
XX
KM Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
KM opiate-mediated ingestive response; opioid activity; analgesic;
KM gastrointestinal motility; respiration; immune system;
KM endocrine system; autonomous nervous system; peristalsis regulator;
KM body weight; neuroendocrine disorder; MOR-1H; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 18..1217
FT /*tag= a
FT /transl_except= (pos: 1188..1190, aa: Gln)
FT /product= "MOR-1H"
XX
PN WO200004046-A2.
XX
PD 27-JAN-2000.
XX
PE 15-JUL-1999; 99MO-US15974.
XX
PR 16-JUL-1998; 98US-0092980.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Pasternak G, Pan Y;
XX
DR WPI; 2000-182402/16.
DR P-PSDB; Y68881.
XX
PT New splice variants of the mu-opioid receptor, useful in screening for
PT selective analgesics and for regulating morphine analgesia or body
PT weight -
XX
PS Claim 40; Fig 2D; 83pp; English.

CC The present sequence encodes a murine mu-opioid receptor (MOR-1)
CC splice variant MOR-1H. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.

CC The present sequence encodes a murine mu-opioid receptor (MOR-1)
CC splice variant MOR-1D. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for

CC The present sequence encodes a murine mu-opioid receptor (MOR-1)
CC splice variant MOR-1B I. The specification describes 11 new exons from
CC the MOR-1 gene, which combine to yield 15 novel splice variants of

CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomic nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.

XX Sequence 1346 BP; 338 A; 398 C; 282 G; 328 T; 0 other;

Query Match 3.7%; Score 59; DB 21; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACCAACATCTACATTTTCACCTTGCTGCGAGATGCTTAGCCAC 597
|||||
DB 361 atgaagactgccacacacatctacatttcaaccttgctgctgcagatgcttagccac 419

RESULT 23

ID 260736 260736 standard; cDNA; 1365 BP.

AC 260736;

DT 16-MAY-2000 (first entry)

XX cDNA encoding murine mu-opioid receptor splice variant MOR-1A.

DE Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;

KW opioid-mediated ingestive response; opioid activity; analgesic;

KM gastrointestinal motility; respiration; immune system;

KW endocrine system; autonomic nervous system; peristalsis regulator;

KM body weight; neuroendocrine disorder; MOR-1A; ss.

OS Mus sp.

XX Key Location/Qualifiers

FT CDS 67..1239

FT /tag= a

FT /product= "MOR-1A"

PN MO200004046-A2.

XX 27-JAN-2000.

XX 15-JUL-1999; 99WO-US15974.

XX 16-JUL-1998; 98US-0092980.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Pasternak G, Pan Y;

XX MPI: 2000-182402/16.

XX P-PSDB; Y68885.

XX New splice variants of the mu-opioid receptor, useful in screening for

XX selective analgesics and for regulating morphine analgesia or body

XX weight -

XX Claim 44; Fig 2J; 83pp; English.

XX The present sequence encodes a murine mu-opioid receptor (MOR-1)

XX splice variant MOR-1A. The specification describes 11 new exons for

CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomic nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.

XX Sequence 1365 BP; 341 A; 399 C; 290 G; 335 T; 0 other;

Query Match 3.7%; Score 59; DB 21; Length 1365;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACCAACATCTACATTTTCACCTTGCTGCGAGATGCTTAGCCAC 597
|||||
DB 361 atgaagactgccacacacatctacatttcaaccttgctgctgcagatgcttagccac 419

RESULT 24

ID 260726 260726 standard; cDNA; 1423 BP.

AC 260726;

DT 16-MAY-2000 (first entry)

XX cDNA encoding murine mu-opioid receptor splice variant MOR-1C.

DE Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;

KW opioid-mediated ingestive response; opioid activity; analgesic;

KM gastrointestinal motility; respiration; immune system;

KW endocrine system; autonomic nervous system; peristalsis regulator;

KM body weight; neuroendocrine disorder; MOR-1C; ss.

OS Mus sp.

XX Key Location/Qualifiers

FT CDS 67..1383

FT /tag= a

FT /product= "MOR-1C"

PN MO200004046-A2.

XX 27-JAN-2000.

XX 15-JUL-1999; 99WO-US15974.

XX 16-JUL-1998; 98US-0092980.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Pasternak G, Pan Y;

XX MPI: 2000-182402/16.

XX P-PSDB; Y68877.

XX New splice variants of the mu-opioid receptor, useful in screening for

XX selective analgesics and for regulating morphine analgesia or body

XX weight -

XX Claim 30; Fig 2A; 83pp; English.

XX The present sequence encodes a murine mu-opioid receptor (MOR-1)

XX splice variant MOR-1C. The specification describes 11 new exons for

CC splice variant MOR-1C. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomic nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
SQ Sequence 1423 BP; 343 A; 423 C; 317 G; 340 T; 0 other;

Query Match 3.7%; Score 59; DB 21; Length 1423;
Best Local Similarity 100.0%; Pred.No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGATGCTTAGCCAC 597
|||||
Db 361 atgaagactgccaccacacatctacatttcaacctgtctgcagatgcttagccac 419

RESULT 25
260729
ID 260729 standard; cDNA: 1542 BP.
XX
AC 260729;
XX
DT 16-MAY-2000 (first entry)
XX
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1E.
XX
XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
XX opioid-mediated ingestive response; opioid activity; analgesic;
XX gastrointestinal motility; respiration; immune system;
XX endocrine system; autonomic nervous system; peristalsis regulator;
XX body weight; neuroendocrine disorder; MOR-1E; ss.
XX
XX Mus sp.
XX
OS
XX
FH Key Location/Qualifiers
FT CDS 67..1272
FT /*tag= a
FT /transl_except= (pos: 772..774, aa: Val)
FT /product= "MOR-1E"
XX
XX MO200004046-A2.
XX
XX 27-JAN-2000.
XX
XX 15-JUL-1999; 99MO-US15974.
XX
XX 16-JUL-1998; 98US-0092980.
XX
XX (SLOK) SLOAN KETTERING INST CANCER RES.
XX
XX Pasternak G, Pan Y;
XX
XX WPI: 2000-182402/16.
XX
XX P-PSDB; Y68880.
XX
XX New splice variants of the mu-opioid receptor, useful in screening for
XX selective analgesics and for regulating morphine analgesia or body
XX weight -
XX
XX Claim 34; Fig 2C; 83pp; English.

XX
CC The present sequence encodes a murine mu-opioid receptor (MOR-1)
CC splice variant MOR-1E. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomic nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be
CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
SQ Sequence 1542 BP; 369 A; 453 C; 346 G; 374 T; 0 other;

Query Match 3.7%; Score 59; DB 21; Length 1542;
Best Local Similarity 100.0%; Pred.No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACACATCTACATTTTCAACCTGCTGGCAGATGCTTAGCCAC 597
|||||
Db 361 atgaagactgccaccacacatctacatttcaacctgtctgcagatgcttagccac 419

RESULT 26
260741
ID 260741 standard; cDNA: 1610 BP.
XX
AC 260741;
XX
DT 16-MAY-2000 (first entry)
XX
DE cDNA encoding murine mu-opioid receptor splice variant MOR-1.
XX
XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
XX opioid-mediated ingestive response; opioid activity; analgesic;
XX gastrointestinal motility; respiration; immune system;
XX endocrine system; autonomic nervous system; peristalsis regulator;
XX body weight; neuroendocrine disorder; MOR-1; ss.
XX
XX Mus sp.
XX
OS
XX
FH Key Location/Qualifiers
FT CDS 283..1479
FT /*tag= a
FT /transl_except= (pos: 916..918, aa: Gly)
FT /product= "MOR-1"
XX
XX MO200004046-A2.
XX
XX 27-JAN-2000.
XX
XX 15-JUL-1999; 99MO-US15974.
XX
XX 16-JUL-1998; 98US-0092980.
XX
XX (SLOK) SLOAN KETTERING INST CANCER RES.
XX
XX Pasternak G, Pan Y;
XX
XX WPI: 2000-182402/16.
XX
XX P-PSDB; Y68889.
XX
XX New splice variants of the mu-opioid receptor, useful in screening for
XX selective analgesics and for regulating morphine analgesia or body
XX weight -
XX
XX

CC to a different pattern of neurons than did DOR-1 and showed greater

CC labeling of the striatum. The identity of DOR-2 (mMOR-1) as that of
CC a mu receptor was confirmed.
XX
SQ Sequence 1981 BP; 499 A; 549 C; 436 G; 496 T; 1 other;

Query Match 3.7%; Score 59; DB 15; Length 1981;
Best Local Similarity 100.0%; Pred. No. 1,2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACACATCTACATTTTCAACCTTGCTGGCAGATGCCCTTAGCCAC 597
|||||
Db 550 atgaagactgccaccaacatctacatttcaaccttgctgcagatgaccttagccac 608

RESULT 29

ID 260735 standard; CDNA; 2045 BP.

XX AC 260735;

DT 16-MAY-2000 (first entry)

XX CDNA encoding murine mu-opioid receptor splice variant MOR-1B II.

XX Mu-opioid receptor; MOR-1; splice variant; morphine analgesia;
KW opioid-mediated ingestive response; opioid activity; analgesic;
KW gastrointestinal motility; respiration; immune system;
KW endocrine system; autonomic nervous system; peristalsis regulator;
KW body weight; neuroendocrine disorder; MOR-1B II; ss.

XX OS Mus sp.

XX Key Location/Qualifiers
FH 67..1296
FT CDS /*tag= a

FT /transl_except= (Pos: 601..603, aa: GLY)
FT /product= "MOR-1B II"

XX W0200004046-A2.

XX 27-JAN-2000.

XX 15-JUL-1999; 99WO-US15974.

XX 16-JUL-1998; 98US-0092980.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Pasternak G, Pan Y;

XX WPI: 2000-182402/16.

XX P-PSDB: Y68887.

XX New splice variants of the mu-opioid receptor, useful in screening for
PT selective analgesics and for regulating morphine analgesia or body
PT weight

XX Claim 42; Fig 2H; 83pp; English.

XX The present sequence encodes a murine mu-opioid receptor (MOR-1)
CC splice variant MOR-1B II. The specification describes 11 new exons for
CC the MOR-1 gene, which combine to yield 15 novel splice variants of
CC the MOR-1 gene. These splice variants are potential targets for
CC modulating morphine analgesia and opioid-mediated ingestive responses.
CC The MOR-1 polypeptide is used to screen compounds for opioid activity.
CC Such compounds are potential analgesics or more generally agents that
CC affect gastrointestinal motility, respiration or the immune, endocrine
CC or autonomic nervous systems, e.g. regulators of peristalsis.
CC Antagonists, agonists and ligands of MOR-1, as well as DNA vectors
CC expressing MOR-1-encoding nucleic acids, or sequences antisense to
CC MOR-1 nucleic acids, are used to regulate morphine analgesia and body
CC weight. The level of MOR-1 or tissue distribution of MOR-1 can be

CC measured to diagnose MOR-1 related pharmacological abnormalities or
CC neuroendocrine disorders, particularly inherited disorders. Transgenic
CC animals with extra copies of the MOR-1 gene, or with endogenous alleles
CC deleted, are used to study loss or gain of function phenotypes.
XX
SQ Sequence 2045 BP; 521 A; 526 C; 422 G; 576 T; 0 other;

Query Match 3.7%; Score 59; DB 21; Length 2045;
Best Local Similarity 100.0%; Pred. No. 1,2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACACATCTACATTTTCAACCTTGCTGGCAGATGCCCTTAGCCAC 597
|||||
Db 361 atgaagactgccaccaacatctacatttcaaccttgctgcagatgaccttagccac 419

RESULT 30

ID V49252 standard; DNA; 2229 BP.

XX AC V49252;

DT 28-OCT-1998 (first entry)

XX Mouse mu opiate receptor gene.

XX Mouse; mu opiate receptor; transgenic animal; mammal; identification;
KW exon; nervous tissue; pain; drug addiction; transplant rejection;
KW immunosuppressant; analgesic; morphine; side effect; ds.

XX OS Mus sp.

XX Key Location/Qualifiers
FH 256..1452
FT CDS /*tag= a

FT /product= "mu opiate receptor"

XX W09802534-A2.

XX 22-JAN-1998.

XX 11-JUL-1997; 97WO-FR01282.

XX 15-JUL-1996; 96FR-0008810.

XX (CNRS) CENT NAT RECH SCI.

XX Dierich A, Kieffer BL, Lemer M, Matthes HMD, Simonin FH;

XX WPI: 1998-110582/10.

XX P-PSDB: W4937.

XX Transgenic animals defective in one type of opioid receptor - used
PT to identify agents for treatment of pain, drug addiction and
PT transplant rejection, lacking side effects of known opiates)

XX Disclosure: Fig 11; 58pp; French.

XX This sequence represents the gene encoding the mouse mu opiate receptor
CC protein. The sequence is used to generate a transgenic non-human mammal
CC for identifying agents for treating disorders associated with opiate
CC receptors. In the mammal, the expression of the gene encoding the opiate
CC receptor is modified, particularly by the deletion of an exon and/or
CC insertion of a marker gene, e.g. the neomycin resistance gene, into the
CC sequence. Especially the expression of the gene is altered in nervous
CC tissue. The agents are potentially useful for treating severe pain
CC (chronic or acute), drug addiction and/or prevention or treatment of
CC transplant rejection (as immunosuppressants). The method may isolate and
CC identify powerful analgesics that lack morphine-like side effects.
SQ Sequence 2229 BP; 562 A; 608 C; 489 G; 570 T; 0 other;

Query Match 3.7%; Score 59; DB 19; Length 2229;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCTGGAGATGCCCTTAGCCAC 597
|||||
Db 550 atgaagactgcacacacatctacattttcaacctgtctgtgcagatgacctagccac 608

RESULT 31

ID 089222 standard; cDNA; 1618 BP.

AC 089222;

DT 20-OCT-1995 (first entry)

DE Rat mu opioid receptor cDNA.

KW Mu opioid receptor; MOR-1; gene therapy; diagnostic; ss.

OS Rattus sp.

Key Location/Qualifiers
FH 214..1410
FT CDS /*tag= a

PN W09507983-A.

PD 23-MAR-1995.

PF 13-SEP-1994; 94WO-US10358.

PR 13-SEP-1993; 93US-0120601.

PA (INDV) UNIV INDIANA FOUND.

PI Yu L;

WP1: 1995-131351/17.

DR P-PSDB; R71964.

XX New nucleic acid encoding new human mu opioid receptor - and
PT related vectors, transformed cells, antibodies etc., useful in
PT diagnosis, treatment and drug screening.

PS Disclosure: Page #90-194; 266pp; English.

CC A 365 bp fragment of the mouse delta opioid receptor was used to
CC screen a rat brain cDNA library under low stringency conditions.
CC One positive clone included the sequence given in 089222, encoding a
CC mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in
CC transfected CHO cells.

XX Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 other;

Query Match 2.9%; Score 47; DB 16; Length 1618;

Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCTGGAGAG 585
|||||
Db 508 atgaagactgcacacacatctacattttcaacctgtctgtgcagaga 554

RESULT 32

ID 089223

AC 089223 standard; cDNA; 1618 BP.

XX 089223;

DT 20-OCT-1995 (first entry)

DE Transcription regulatory protein cDNA.

KW Mu opioid receptor; MOR-1; gene therapy; diagnostic;

OS transcriptions regulatory protein; ss.

XX Rattus sp.

Key Location/Qualifiers
FH 339..1235
FT CDS /*tag= a

PN W09507983-A.

PD 23-MAR-1995.

PF 13-SEP-1994; 94WO-US10358.

PR 13-SEP-1993; 93US-0120601.

PA (INDV) UNIV INDIANA FOUND.

PI Yu L;

WP1: 1995-131351/17.

DR P-PSDB; R71965.

XX New nucleic acid encoding new human mu opioid receptor - and
PT related vectors, transformed cells, antibodies etc., useful in
PT diagnosis, treatment and drug screening.

PS Disclosure: Page 199-203; 266pp; English.

CC A 365 bp fragment of the mouse delta opioid receptor was used to
CC screen a rat brain cDNA library under low stringency conditions.
CC One positive clone included the sequence given in 089222, encoding a
CC mu opioid receptor, MOR-1 (R71964). Sequence analysis revealed an
CC alternative reading frame (089223) encoding a zinc
CC finger-containing transcription regulatory protein (R71965).

XX Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T; 0 other;

Query Match 2.9%; Score 47; DB 16; Length 1618;

Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCTGGAGAG 585
|||||
Db 508 atgaagactgcacacacatctacattttcaacctgtctgtgcagaga 554

RESULT 33

ID 079199 standard; cDNA; 2070 BP.

AC 079199;

DT 19-APR-1995 (first entry)

DE Rat mu-subtype opioid receptor cDNA.

KW Mu-subtype opioid receptor; MSOR; drug addiction; ds.

OS Rattus rattus.

Key Location/Qualifiers
FH 83..1154
FT CDS /*tag= a

FT /product- Mu-subtype_opioid_receptor

PN EP612845-A.

XX 31-AUG-1994.
PD 09-FEB-1994; 94EP-0101968.
XX 26-FEB-1993; 93US-0026140.
XX (AMCY) AMERICAN CYANAMID CO.
PA Corbett MJ, Eppler CM, Shieh H, Zysk JR;
PI MPI; 1994-265963/33.
XX P-PSDB; R65188.
DR
XX
PT Pure mu-type opioid receptor protein - and nucleic acid coding
PT for it
XX
XX Claim 1; Fig 11; 39pp; English.
PS
XX
CC R65188 is the rat mu-subtype opioid receptor protein purified
CC from rat brain membranes, with biotinyl-b-endorphin (R56666)
CC as its ligand. It is encoded by the nucleotide sequence Q79199
CC which was synthesised using Q71022 and Q71023 as PCR primers.
CC R65188 is useful for identifying other receptor subtypes, for
CC screening new opioid ligands, and for studying mechanisms of
CC opioid action, e.g. drug addiction.
XX
SQ Sequence 2070 BP; 526 A; 564 C; 423 G; 557 T; 0 other;

Query Match 2.9%; Score 47; DB 15; Length 2070;
Best Local Similarity 100.0%; Pred. No. 1.le-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAGACTGCCACCATCTACATTTTCACCTTGCTCTGCGAGA 585
|||||
Db 260 atgaagactgcaccacacatctacatttcaacctgtgctgcgcaga 306

Search completed: November 14, 2000, 23:44:09
Job time: 3647 sec

THE N.C. BANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2000, 21:37:45 ; Search time 839.19 Seconds
(without alignments)
11861.817 Million cell updates/sec

Title: US-08-305-518-7

Perfect score: 1610
Sequence: 1 CGGATGACGCTCTGTGACT.....GCTCTGCACATTAGAGCCG 1610

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 7189864 seqs, 3091403243 residues

Word size : 35

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
27: gb_est27:*
28: gb_est28:*
29: gb_est29:*
30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: em_estba:*
42: em_estfun:*
43: em_esthum1:*

44: em_esthum2:*
45: em_esthum3:*
46: em_esthum4:*
47: em_esthum5:*
48: em_esthum6:*
49: em_esthum7:*
50: em_esthum8:*
51: em_esthum9:*
52: em_esthum10:*
53: em_esthum11:*
54: em_esthum12:*
55: em_esthum13:*
56: em_esthum14:*
57: em_esthum15:*
58: em_esthum16:*
59: em_esthum17:*
60: em_esthum18:*
61: em_esthum19:*
62: em_esthum20:*
63: em_estin1:*
64: em_estin2:*
65: em_estin3:*
66: em_estin4:*
67: em_estom:*
68: em_estrov1:*
69: em_estrov2:*
70: em_estp11:*
71: em_estp12:*
72: em_estp13:*
73: em_estp14:*
74: em_estp15:*
75: em_estro1:*
76: em_estro2:*
77: em_estro3:*
78: em_estro4:*
79: em_estro5:*
80: em_estro6:*
81: em_estro7:*
82: em_estro8:*
83: em_estro9:*
84: em_estro10:*
85: em_estro11:*
86: em_estro12:*
87: em_estro13:*
88: gb_gss1:*
89: gb_gss2:*
90: gb_gss3:*
91: gb_gss4:*
92: em_gss1:*
93: em_gss2:*
94: em_gss3:*
95: em_gss4:*
96: gb_gss5:*
97: gb_gss6:*
98: gb_gss7:*
99: gb_gss8:*
100: gb_gss9:*
101: gb_gss10:*
102: gb_gss11:*
103: gb_gss12:*
104: gb_gss13:*
105: gb_gss14:*
106: gb_gss15:*
107: gb_gss16:*
108: gb_gss17:*
109: gb_gss18:*
110: gb_gss19:*
111: gb_gss20:*
112: gb_gss21:*
113: gb_gss22:*
114: gb_gss23:*
115: gb_gss24:*
116: em_gss5:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

```

117: em_gsa6:*
118: em_gsa7:*
119: em_gsa8:*
120: em_gsa9:*
121: em_gsa10:*
122: em_gsa11:*
123: em_gsa12:*
124: em_gsa13:*
125: em_gsa14:*
126: em_gsa15:*
127: em_gsa16:*

```

Result No.	Score	Query Match	Length	ID	Description
C 1	207	12.9	520	111 B82759	B82759 RPCI11-17K2
C 2	85	5.3	245	98 A0488720	A0488720 RPCI-11-2

ALIGNMENTS

RESULT 1
B82759/c
LOCUS B82759 520 bp DNA GSS 09-APR-1999
DEFINITION RPCI11-17K22.TP RPCI-11 Homo sapiens genomic clone RPCI-11-17K22,
DNA sequence.
ACCESSION B82759
VERSION B82759.1 GI:2869782
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 520)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: RPCI11-17K22.TVB
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@jeong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES

source 1.520
/organism="Homo sapiens"
/db_xref="GDB:7506405"
/db_xref="taxon:9606"
/clone="RPCI-11-17K22"
/clone_11b="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"

BASE COUNT 101 a 154 c 153 g 112 t
ORIGIN

Query Match 12.9%; Score 207; DB 111; Length 520;
Best Local Similarity 100.0%; Pred. No. 6.4e-102;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	322	CGGTTCCGGGTCACATGTCCTAGATAGGACACCTGTCGACCCATCGGTCGAA	381
Db	387	CGGTTCCGGGTCACATGTCCTAGATAGGACACCTGTCGACCCATCGGTCGAA	328
QY	382	CCGACCGACCTGGCGCGGAGAGACACCTGTGCTCCGACCGAGTCCCTCATGAT	441
Db	327	CCGACCGACCTGGCGCGGAGAGACACCTGTGCTCCGACCGAGTCCCTCATGAT	268
QY	442	CACGGCCATCAGATCATGCGCCCTCTACTCATGTGTGCGGGGCTCTTCGAAA	501
Db	267	CACGGCCATCAGATCATGCGCCCTCTACTCATGTGTGCGGGGCTCTTCGAAA	209
QY	502	CTTCCTGGTCTATGATGATGTCAG	528
Db	207	CTTCCTGGTCTATGATGATGTCAG	181

RESULT 2
A0488720/c
LOCUS A0488720 245 bp DNA GSS 24-APR-1999
DEFINITION RPCI-11-230H7.TV RPCI-11 Homo sapiens genomic clone RPCI-11-230H7,
DNA sequence.
ACCESSION A0488720
VERSION A0488720.1 GI:4674594
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 245)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: RPCI-11-230H7.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@jeong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES

source 1.245
/organism="Homo sapiens"
/db_xref="GDB:7588110"
/db_xref="taxon:9606"
/clone="RPCI-11-230H7"
/clone_11b="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"

BASE COUNT 49 a 82 c 61 g 53 t
ORIGIN

Query Match 5.38; Score 85; DB 98; Length 245;
Best Local Similarity 100.0%; Pred. No. 4.1e-35;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 444 CGGCATCAGCATGAGCCCTCTACTCATCATGTGCGTGGGCTCTTCGAAACT 503
|||||
Db 194 CGGCATCAGCATGAGCCCTCTACTCATCATGTGCGTGGGCTCTTCGAAACT 135
|||||

QY 504 TCCTGTCATGTATGATTTGTCAG 528
|||||
Db 134 TCCTGTCATGTATGATTTGTCAG 110
|||||

Search completed: November 14, 2000, 23:06:57
Job time: 5352 sec

601 TACCTGCTCCAGAGTGTGAATTAACCTTAAGGAACATGGCCATTGGACCATCT 660
601 TACCTGCTCCAGAGTGTGAATTAACCTTAAGGAACATGGCCATTGGACCATCT 660
661 TTGCAAGATAGTATCTCCATAGATTAATACATGTTCCACGACATATTCACCTCTG 720
661 TTGCAAGATAGTATCTCCATAGATTAATACATGTTCCACGACATATTCACCTCTG 720
721 CACCATAGAGTGTGAATTAACCTTAAGGAACATGGCCATTGGACCATCT 780
721 CACCATAGAGTGTGAATTAACCTTAAGGAACATGGCCATTGGACCATCT 780
781 TACCTGCTCCAGAGTGTGAATTAACCTTAAGGAACATGGCCATTGGACCATCT 840
781 TACCTGCTCCAGAGTGTGAATTAACCTTAAGGAACATGGCCATTGGACCATCT 840
841 TCTTCTGTAATGTTCATAGGCTTACACAAATATACAGCAAGGTTCCATAGATGTAC 900
841 TCTTCTGTAATGTTCATAGGCTTACACAAATATACAGCAAGGTTCCATAGATGTAC 900
901 AACATTTCTCATACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
901 AACATTTCTCATACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
961 CGCCTTCAATATGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
961 CGCCTTCAATATGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
1021 CAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
1021 CAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
1081 CAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
1081 CAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
1141 CGTCTCATTAATGAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
1141 CGTCTCATTAATGAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
1201 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
1201 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
1261 GGATGAAGATCTCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
1261 GGATGAAGATCTCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
1321 GCAACAAAGCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
1321 GCAACAAAGCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
1381 AGTGTGATAGATTAATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
1381 AGTGTGATAGATTAATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
1441 ACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
1441 ACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
1501 AGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
1501 AGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
1561 CATTCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
1561 CATTCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620

RESULT 2
PCT-US94-10358-7
; Sequence 7, Application PC/TUS9410358

GENERAL INFORMATION:
APPLICANT: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
TITLE OF INVENTION: 17
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/120,601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US94-10358-7

Query Match 100.0%; Score 1610; DB 6; Length 1610;
Best local Similarity 100.0%; Pred. No. 0;
Matches 1610; Conservative 0; Mismatches 0; Indels 0; Gaps 0

61 ATGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
61 ATGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
61 ATGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
121 GTAAGAAACAGCAGAGCTGTGCGAGCGGCGAAAGAGAGCGGCTGAGCGCTTGAACCC 180
121 GTAAGAAACAGCAGAGCTGTGCGAGCGGCGAAAGAGAGCGGCTGAGCGCTTGAACCC 180
181 GAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
181 GAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
241 GAGACAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
241 GAGACAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
301 TTGCTCCCAAGCAGCAGCCCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
301 TTGCTCCCAAGCAGCAGCCCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
361 GTCCGACCCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
361 GTCCGACCCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

GENERAL INFORMATION:
APPLICANT: Yu, Lei
TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,108
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (cDNA)
FEATURE:
NAME/KEY: CDS
LOCATION: 214..1410
US-08-889-108-1

Query Match 2.9%; Score 47; DB 5; Length 1618;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCGAGA 585
|||||
DB 508 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCGAGA 554

RESULT 5
US-08-889-108-3
Sequence 3, Application US/08889108
Patent No. 6103492
GENERAL INFORMATION:
APPLICANT: Yu, Lei
TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/889,108
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (cDNA)
FEATURE:
NAME/KEY: CDS
LOCATION: 339..1235
US-08-889-108-3

Query Match 2.9%; Score 47; DB 5; Length 1618;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCGAGA 585
|||||
DB 508 ATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTGCGAGA 554

RESULT 6
PCT-US94-10358-1
Sequence 1, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120,601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 214..1410
PCT-US94-10358-1

Query Match 2.9%; Score 47; DB 6; Length 1618;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAGACTGCCACCACTCTACATTTTCACACCTTGCTCTGCGAGA 585
|||||
Db 508 ATGAGACTGCCACCACTCTACATTTTCACACCTTGCTCTGCGAGA 554

RESULT 7

PCT-US94-10358-3
Sequence 3, Application PC/TUS9410358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10358
FILING DATE: Concurrently herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120.601
FILING DATE: 13 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA005P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 339..1235
PCT-US94-10358-3

Query Match 2.9%; Score 47; DB 6; Length 1618;
Best Local Similarity 100.0%; Pred. No. 2.5e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 539 ATGAGACTGCCACCACTCTACATTTTCACACCTTGCTCTGCGAGA 585
|||||
Db 508 ATGAGACTGCCACCACTCTACATTTTCACACCTTGCTCTGCGAGA 554

